

μL of the diluted conjugate was added to each well and incubated for 30 minutes at room temperature. Following incubation, the wells were washed five times with PBS/0.1% Tween 20™. 100 μL of tetramethylbenzidine peroxidase (TMB) substrate (Kirkegaard and Perry Laboratories, Gaithersburg, MD) was added, undiluted, and 5 incubated for about 15 minutes. The reaction was stopped with the addition of 100 μL of 1 N H<sub>2</sub>SO<sub>4</sub> to each well, and the plates were read at 450 nm.

Figure 4 shows the ELISA reactivity of two recombinant antigens isolated using method A in Example 3 (TbRa3 and TbRa9) with sera from *M. tuberculosis* positive and negative patients. The reactivity of these antigens is 10 compared to that of bacterial lysate isolated from *M. tuberculosis* strain H37Ra (Difco, Detroit, MI). In both cases, the recombinant antigens differentiated positive from negative sera. Based on cut-off values obtained from receiver-operator curves, TbRa3 detected 56 out of 87 positive sera, and TbRa9 detected 111 out of 165 positive sera.

Figure 5 illustrates the ELISA reactivity of representative antigens 15 isolated using method B of Example 3. The reactivity of the recombinant antigens TbH4, TbH12, Tb38-1 and the peptide TbM-1 (as described in Example 4) is compared to that of the 38 kD antigen described by Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989. Again, all of the polypeptides tested differentiated positive from negative sera. Based on cut-off values obtained from receiver-operator curves, TbH4 20 detected 67 out of 126 positive sera, TbH12 detected 50 out of 125 positive sera, 38-1 detected 61 out of 101 positive sera and the TbM-1 peptide detected 25 out of 30 positive sera.

The reactivity of four antigens (TbRa3, TbRa9, TbH4 and TbH12) with sera from a group of *M. tuberculosis* infected patients with differing reactivity in the acid fast stain of sputum (Smithwick and David, *Tubercle* 52:226, 1971) was also 25 examined, and compared to the reactivity of *M. tuberculosis* lysate and the 38 kD antigen. The results are presented in Table 3, below:

**TABLE 3**  
**REACTIVITY OF ANTIGENS WITH SERA FROM *M. TUBERCULOSIS* PATIENTS**

Patient	Acid Fast Sputum	ELISA Values					
		Lysate	38KD	TbRa9	TbH12	TbH4	TbRa3
Tb01B93I-2	++++	1.853	0.634	0.998	1.022	1.030	1.314
Tb01B93I-19	++++	2.657	2.322	0.608	0.837	1.857	2.335
Tb01B93I-8	++	2.703	0.527	0.492	0.281	0.501	2.002
Tb01B93I-10	++	1.665	1.301	0.685	0.216	0.448	0.458
Tb01B93I-11	++	2.817	0.697	0.509	0.301	0.173	2.608
Tb01B93I-15	++	1.28	0.283	0.808	0.218	1.537	0.811
Tb01B93I-16	+++	2.908	>3	0.899	0.441	0.593	1.680
Tb01B93I-25	++	0.395	0.131	0.335	0.211	0.107	0.948
Tb01B93I-37	+++	2.653	2.432	2.282	0.977	1.221	0.857
Tb01B93I-89	—	1.912	2.370	2.436	0.876	0.520	0.952
Tb01B94I-108	—	1.639	0.341	0.797	0.368	0.654	0.798
Tb01B94I-201	—	1.721	0.419	0.661	0.137	0.064	0.692
Tb01B93I-88	—	1.939	1.269	2.519	1.381	0.214	0.530
Tb01B93I-92	—	2.385	2.329	2.78	0.685	0.997	2.527
Tb01B94I-109	+	0.993	0.620	0.574	0.441	0.5	2.558
Tb01B94I-210	++	2.777	>3	0.393	0.367	1.004	1.315
Tb01B94I-224	++	2.913	0.476	0.251	1.297	1.990	0.256
Tb01B93I-9	-	2.649	0.278	0.210	0.140	0.181	1.586
Tb01B93I-14	+	>3	1.538	0.282	0.291	0.549	2.880
Tb01B93I-21	-	2.645	0.739	2.499	0.783	0.536	1.770

Patient	Acid Fast Sputum	ELISA Values					
		Lysate	38kD	TbRa9	TbH12	TbH4	TbRa3
Tb01B93I-22	+	0.714	0.451	2.082	0.285	0.269	1.159
Tb01B93I-31	+	0.956	0.490	1.019	0.812	0.176	1.293
Tb01B93I-32	-	2.261	0.786	0.668	0.273	0.535	0.405
Tb01B93I-52	-	0.658	0.114	0.434	0.320	0.273	1.140
Tb01B93I-99	-	2.118	0.584	1.62	0.119	0.977	0.729
Tb01B94I-130	-	1.349	0.224	0.86	0.282	0.383	2.146
Tb01B94I-131	-	0.685	0.324	1.173	0.059	0.118	1.431
AT4-0070	Normal	0.072	0.043	0.092	0.071	0.040	0.039
AT4-0105	Normal	0.397	0.121	0.118	0.103	0.078	0.390
3/15/94-1	Normal	0.227	0.064	0.098	0.026	0.061	0.228
4/15/93-2	Normal	0.114	0.240	0.071	0.034	0.041	0.264
5/26/94-4	Normal	0.089	0.259	0.096	0.046	0.008	0.053
5/26/94-3	Normal	0.139	0.093	0.085	0.019	0.067	0.61

Based on cut-off values obtained from receiver-operator curves, TbRa3 detected 23 out of 27 positive sera, TbRa9 detected 22 out of 27, TbH4 detected 18 out of 27 and TbH12 detected 15 out of 27. If used in combination, these four antigens would have a theoretical sensitivity of 27 out of 27, indicating that these antigens should complement each other in the serological detection of *M. tuberculosis* infection. In addition, several of the recombinant antigens detected positive sera that were not detected using the 38 kD antigen, indicating that these antigens may be complementary to the 38 kD antigen.

The reactivity of the recombinant antigen TbRa11 with sera from *M. tuberculosis* patients shown to be negative for the 38 kD antigen, as well as with sera from PPD positive and normal donors, was determined by ELISA as described above.

The results are shown in Figure 6 which indicates that TbRa11, while being negative with sera from PPD positive and normal donors, detected sera that were negative with the 38 kD antigen. Of the thirteen 38 kD negative sera tested, nine were positive with TbRa11, indicating that this antigen may be reacting with a sub-group of 38 kD antigen negative sera. In contrast, in a group of 38 kD positive sera where TbRa11 was reactive, the mean OD 450 for TbRa11 was lower than that for the 38 kD antigen. The data indicate an inverse relationship between the presence of TbRa11 activity and 38 kD positivity.

The antigen TbRa2A was tested in an indirect ELISA using initially 50 µl of serum at 1:100 dilution for 30 minutes at room temperature followed by washing in PBS Tween and incubating for 30 minutes with biotinylated Protein A (Zymed, San Francisco, CA) at a 1:10,000 dilution. Following washing, 50 µl of streptavidin-horseradish peroxidase (Zymed) at 1:10,000 dilution was added and the mixture incubated for 30 minutes. After washing, the assay was developed with TMB substrate as described above. The reactivity of TbRa2A with sera from *M. tuberculosis* patients and normal donors is shown in Table 4. The mean value for reactivity of TbRa2A with sera from *M. tuberculosis* patients was 0.444 with a standard deviation of 0.309. The mean for reactivity with sera from normal donors was 0.109 with a standard deviation of 0.029. Testing of 38 kD negative sera (Figure 7) also indicated that the TbRa2A antigen was capable of detecting sera in this category.

TABLE 4  
REACTIVITY OF TBRA2A WITH SERA FROM *M. TUBERCULOSIS* PATIENTS AND FROM  
 NORMAL DONORS

28

Serum ID	Status	OD 450
Tb85	TB	0.680
Tb86	TB	0.450
Tb87	TB	0.263
Tb88	TB	0.275
Tb89	TB	0.403
Tb91	TB	0.393
Tb92	TB	0.401

Tb93	TB	0.232
Tb94	TB	0.333
Tb95	TB	0.435
Tb96	TB	0.284
Tb97	TB	0.320
Tb99	TB	0.328
Tb100	TB	0.817
Tb101	TB	0.607
Tb102	TB	0.191
Tb103	TB	0.228
Tb107	TB	0.324
Tb109	TB	1.572
Tb112	TB	0.338
DL4-0176	Normal	0.036
AT4-0043	Normal	0.126
AT4-0044	Normal	0.130
AT4-0052	Normal	0.135
AT4-0053	Normal	0.133
AT4-0062	Normal	0.128
AT4-0070	Normal	0.088
AT4-0091	Normal	0.108
AT4-0100	Normal	0.106
AT4-0105	Normal	0.108
AT4-0109	Normal	0.105

The reactivity of the recombinant antigen (g) (SEQ ID NO: 60) with sera from *M. tuberculosis* patients and normal donors was determined by ELISA as described above. Figure 8 shows the results of the titration of antigen (g) with four *M. tuberculosis* positive sera that were all reactive with the 38 kD antigen and with four donor sera. All four positive sera were reactive with antigen (g).

The reactivity of the recombinant antigen TbH-29 (SEQ ID NO: 137) with sera from *M. tuberculosis* patients, PPD positive donors and normal donors was determined by indirect ELISA as described above. The results are shown in Figure 9. TbH-29 detected 30 out of 60 *M. tuberculosis* sera, 2 out of 8 PPD positive sera and 2 out of 27 normal sera.

Figure 10 shows the results of ELISA tests (both direct and indirect) of the antigen TbH-33 (SEQ ID NO: 140) with sera from *M. tuberculosis* patients and from normal donors and with a pool of sera from *M. tuberculosis* patients. The mean

OD 450 was demonstrated to be higher with sera from *M. tuberculosis* patients than from normal donors, with the mean OD 450 being significantly higher in the indirect ELISA than in the direct ELISA. Figure 11 is a titration curve for the reactivity of recombinant TbH-33 with sera from *M. tuberculosis* patients and from normal donors showing an increase in OD 450 with increasing concentration of antigen.

The reactivity of the recombinant antigens RDIF6, RDIF8 and RDIF10 (SEQ ID NOS: 184-187, respectively) with sera from *M. tuberculosis* patients and normal donors was determined by ELISA as described above. RDIF6 detected 6 out of 32 *M. tuberculosis* sera and 0 out of 15 normal sera; RDIF8 detected 14 out of 32 *M. tuberculosis* sera and 0 out of 15 normal sera; and RDIF10 detected 4 out of 27 *M. tuberculosis* sera and 1 out of 15 normal sera. In addition, RDIF10 was found to detect 0 out of 5 sera from PPD-positive donors.

The antigens MO-1, MO-2, MO-4, MO-28 and MO-29 described above in Example 5, were expressed in *E. coli* and purified using a hexahistidine tag. The reactivity of these antigens with both *M. tuberculosis* positive and negative sera was examined by ELISA as described above. Titration curves showing the reactivity of MO-1, MO-2, MO-4, MO-28 and MO-29 at different solid phase coat levels when tested against four *M. tuberculosis* positive sera and four *M. tuberculosis* negative sera are shown in Figs. 12A-E, respectively. Three of the clones, MO-1, MO-2 and MO-29 were further tested on panels of HIV positive/tuberculosis (HIV/TB) positive and extrapulmonary sera. MO-1 detected 3/20 extrapulmonary and 2/38 HIV/TB sera. On the same sera groups, MO-2 detected 2/20 and 10/38, and MO-29 detected 2/20 and 8/38 sera. In combination these three clones would have detected 4/20 extrapulmonary sera and 16/38 HIV/TB sera. In addition, MO-1 detected 6/17 sera that had previously been shown only to react with *M. tuberculosis* lysate and not with either 38 kD or with other antigens of the subject invention.

EXAMPLE 10PREPARATION AND CHARACTERIZATION OF M. TUBERCULOSIS FUSION PROTEINS

A fusion protein containing TbRa3, the 38 kD antigen and Tb38-1 was  
5 prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR in order to facilitate their fusion and the subsequent expression of the fusion protein TbRa3-38 kD-Tb38-1. TbRa3, 38 kD and Tb38-1 DNA was used to perform PCR using the primers PDM-64 and PDM-65 (SEQ ID NO: 141 and 142), PDM-57 and  
10 PDM-58 (SEQ ID NO: 143 and 144), and PDM-69 and PDM-60 (SEQ ID NO: 145-  
146), respectively. In each case, the DNA amplification was performed using 10 µl  
10X Pfu buffer, 2 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM  
concentration, 81.5 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA)  
and 1 µl DNA at either 70 ng/µl (for TbRa3) or 50 ng/µl (for 38 kD and Tb38-1). For  
15 TbRa3, denaturation at 94°C was performed for 2 min, followed by 40 cycles of 96°C  
for 15 sec and 72°C for 1 min, and lastly by 72°C for 4 min. For 38 kD, denaturation at  
96°C was performed for 2 min, followed by 40 cycles of 96°C for 30 sec, 68°C for 15  
sec and 72°C for 3 min, and finally by 72°C for 4 min. For Tb38-1 denaturation at 94°  
C for 1 min was followed by 10 cycles of 96°C for 15 sec, 68°C for 15 sec and 72°C for  
20 1.5 min, 30 cycles of 96°C for 15 sec, 64°C for 15 sec and 72°C for 1.5, and finally by  
72°C for 4 min.

The TbRa3 PCR fragment was digested with NdeI and EcoRI and cloned directly into pT7^L2 IL 1 vector using NdeI and EcoRI sites. The 38 kD PCR fragment was digested with Sse8387I, treated with T4 DNA polymerase to make blunt ends and  
25 then digested with EcoRI for direct cloning into the pT7^L2Ra3-1 vector which was digested with SstI and EcoRI. The 38-1 PCR fragment was digested with Eco47III and EcoRI and directly subcloned into pT7^L2Ra3/38KD-17 digested with the same enzymes. The whole fusion was then transferred to pET28b using NdeI and EcoRI sites. The fusion construct was confirmed by DNA sequencing.

The expression construct was transformed to BLR pLys S *E. coli* (Novagen, Madison, WI) and grown overnight in LB broth with kanamycin (30 µg/ml) and chloramphenicol (34 µg/ml). This culture (12 ml) was used to inoculate 500 ml 2XYT with the same antibiotics and the culture was induced with IPTG at an OD<sub>560</sub> of 5 0.44 to a final concentration of 1.2 mM. Four hours post-induction, the bacteria were harvested and sonicated in 20 mM Tris (8.0), 100 mM NaCl, 0.1% DOC, 20 µg/ml Leupeptin, 20 mM PMSF followed by centrifugation at 26,000 X g. The resulting pellet was resuspended in 8 M urea, 20 mM Tris (8.0), 100 mM NaCl and bound to Pro-bond nickel resin (Invitrogen, Carlsbad, CA). The column was washed several times 10 with the above buffer then eluted with an imidazole gradient (50 mM, 100 mM, 500 mM imidazole was added to 8 M urea, 20 mM Tris (8.0), 100 mM NaCl). The eluates containing the protein of interest were then dialyzed against 10 mM Tris (8.0).

The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbRa3-38 kD-Tb38-1) are provided in SEQ ID NO: 147 and 15 148, respectively.

A fusion protein containing the two antigens TbH-9 and Tb38-1 (hereinafter referred to as TbH9-Tb38-1) without a hinge sequence, was prepared using a similar procedure to that described above. The DNA sequence for the TbH9-Tb38-1 fusion protein is provided in SEQ ID NO: 151.

20 A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and DPEP was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified 25 by PCR and cloned into vectors essentially as described above, with the primers PDM-69 (SEQ ID NO:145 and PDM-83 (SEQ ID NO: 200) being used for amplification of the Tb38-1A fragment. Tb38-1A differs from Tb38-1 by a DraI site at the 3' end of the coding region that keeps the final amino acid intact while creating a blunt restriction site that is in frame. The TbRa3/38kD/Tb38-1A fusion was then transferred to pET28b using NdeI and EcoRI sites.

DPEP DNA was used to perform PCR using the primers PDM-84 and 30 PDM-85 (SEQ ID NO: 201 and 202, respectively) and 1 µl DNA at 50 ng/µl.

Denaturation at 94 °C was performed for 2 min, followed by 10 cycles of 96 °C for 15 sec, 68 °C for 15 sec and 72 °C for 1.5 min; 30 cycles of 96 °C for 15 sec, 64 °C for 15 sec and 72 °C for 1.5 min; and finally by 72 °C for 4 min. The DPEP PCR fragment was digested with EcoRI and Eco72I and clones directly into the pET28Ra3/38kD/38-1A construct which was digested with Drai and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-2) are provided in SEQ ID NO: 203 and 204, respectively.

10 A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and TbH4 was prepared as follows.

Genomic *M. tuberculosis* DNA was used to PCR full-length TbH4 (FL TbH4) with the primers PDM-157 and PDM-160 (SEQ ID NO: 343 and 344, respectively) and 2 µl DNA at 100 ng/µl. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 61 °C for 20 sec and 72 °C for 5 min; and finally by annealing at 72 °C for 10 min. The FL TbH4 PCR fragment was digested with EcoRI and Sac I (New England Biolabs.) and cloned directly into the pET28Ra3/38kD/38-1A construct described above which was digested with Drai and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing.

15 Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-6) are provided in SEQ ID NO: 345 and 346, respectively.

A fusion protein containing the antigen 38kD and DPEP separated by a linker was prepared as follows.

20 38 kD DNA was used to perform PCR using the primers PDM-176 and PDM-175 (SEQ ID NO: 347 and 348, respectively), and 1 µl PET28Ra3/38kD/38-1/Ra2A-12 DNA at 110 ng/µl. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 71 °C for 15 sec and 72 °C for 5 min and 40 sec; and finally by annealing at 72 °C for 4 min. The two sets of primers PDM-171, PDM-172, and PDM-173, PDM-174 were annealed by heating to 95 °C for 2 min and

then ramping down to 25 °C slowly at 0.1 °C/sec. DPEP DNA was used to perform PCR as described above. The 38 kD fragment was digested with Eco RI (New England Biolabs) and cloned into a modified pT7AL2 vector which was cut with Eco 72 I (Promega) and Eco RI. The modified pT7AL2 construct was designed to have a 5 MGHHHHHH amino acid coding region in frame just 5' of the Eco 72 I site. The construct was digested with Kpn 2I (Gibco, BRL) and Pst I (New England Biolabs) and the annealed sets of phosphorylated primers (PDM-171, PDM-172 and PDM-173, PDM-174) were cloned in. The DPEP PCR fragment was digested with Eco RI and Eco 72 I and cloned into this second construct which was digested with Eco 47 III (New 10 England Biolabs) and Eco RI. Ligations were done with a ligation kit from Pnivera (Madison, WI). The resulting construct was digested with NdeI (New England Biolabs) and Eco RI, and transferred to a modified pET28 vector. The fusion construct was confirmed to be correct by DNA sequencing.

15 Recombinant protein was prepared essentially as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-8) are provided in SEQ ID NO: 349 and 350, respectively.

#### EXAMPLE 11

20 USE OF *M. TUBERCULOSIS* FUSION PROTEINS FOR  
SERODIAGNOSIS OF TUBERCULOSIS

25 The effectiveness of the fusion protein TbRa3-38 kD-Tb38-1, prepared as described above, in the serodiagnosis of tuberculosis infection was examined by ELISA.

30 The ELISA protocol was as described above in Example 6, with the fusion protein being coated at 200 ng/well. A panel of sera was chosen from a group of tuberculosis patients previously shown, either by ELISA or by western blot analysis, to react with each of the three antigens individually or in combination. Such a panel enabled the dissection of the serological reactivity of the fusion protein to determine if

all three epitopes functioned with the fusion protein. As shown in Table 5, all four sera that reacted with TbRa3 only were detectable with the fusion protein. Three sera that reacted only with Tb38-1 were also detectable, as were two sera that reacted with 38 kD alone. The remaining 15 sera were all positive with the fusion protein based on a cut-off in the assay of mean negatives +3 standard deviations. This data demonstrates the functional activity of all three epitopes in the fusion protein.

10 TABLE 5  
 REACTIVITY OF TRI-PEPTIDE FUSION PROTEIN WITH SERA FROM *M. TUBERCULOSIS*  
 PATIENTS

Serum ID	Status	ELISA and/or Western Blot Reactivity with Individual proteins			Fusion Recombinant OD 450	Fusion Recombinant Status
		38kD	Tb38-1	TbRa3		
01B93I-40	TB	-	-	+	0.413	+
01B93I-41	TB	-	+	+	0.392	+
01B93I-29	TB	+	-	+	2.217	+
01B93I-109	TB	+	+	+	0.522	+
01B93I-132	TB	+	+	+	0.937	+
5004	TB	+	-	+	1.098	+
15004	TB	+	+	+	2.077	+
39004	TB	+	-	+	1.675	+
68004	TB	+	-	+	2.388	+
99004	TB	-	+	+	0.607	+
107004	TB	-	+	+	0.667	+
92004	TB	+	+	+	1.070	+
97004	TB	+	-	+	1.152	+
118004	TB	+	-	+	2.694	+
173004	TB	+	+	+	3.258	+
175004	TB	+	-	+	2.514	+
274004	TB	-	+	+	3.220	+
276004	TB	-	+	+	2.991	+
282004	TB	+	-	+	0.824	+
289004	TB	-	-	+	0.848	+

308004	TB	-	+	-	3.338	+
314004	TB	-	+	-	1.362	+
317004	TB	+	-	-	0.763	+
312004	TB	-	-	+	1.079	+
D176	PPD	-	-	-	0.145	-
D162	PPD	-	-	-	0.073	-
D161	PPD	-	-	-	0.097	-
D27	PPD	-	-	-	0.082	-
A6-124	NORMAL	-	-	-	0.053	-
A6-125	NORMAL	-	-	-	0.087	-
A6-126	NORMAL	-	-	+	0.346	a
A6-127	NORMAL	-	-	-	0.064	-
A6-128	NORMAL	-	-	-	0.034	-
A6-129	NORMAL	-	-	+	0.037	-
A6-130	NORMAL	-	-	-	0.057	-
A6-131	NORMAL	-	-	-	0.054	-
A6-132	NORMAL	-	-	-	0.022	-
A6-133	NORMAL	-	-	-	0.147	-
A6-134	NORMAL	-	-	-	0.101	-
A6-135	NORMAL	-	-	-	0.066	-
A6-136	NORMAL	-	-	-	0.054	-
A6-137	NORMAL	-	-	-	0.063	-
A6-138	NORMAL	-	-	-	0.041	-
A6-139	NORMAL	-	-	-	0.103	-
A6-140	NORMAL	-	-	-	0.212	-
A6-141	NORMAL	-	-	-	0.056	-
A6-142	NORMAL	-	-	-	0.051	-

The reactivity of the fusion protein TbF-2 with sera from *M. tuberculosis*-infected patients was examined by ELISA using the protocol described above. The results of these studies (Table 6) demonstrate that all four antigens function independently in the fusion protein.

TABLE 6  
REACTIVITY OF TbF-2 FUSION PROTEIN WITH TB AND NORMAL SERA

Serum ID	Status	TbF OD450	Status	TbF-2 OD450	Status	ELISA Reactivity			
						38 kD	TbRaJ	TbS-1	DVEP
B931-40	TB	0.57	-	0.321	+	-	-	-	-
B931-41	TB	0.601	+	0.396	+	-	-	-	-
B931-109	TB	0.494	+	0.404	+	+	+	+	+
B931-132	TB	1.502	-	1.392	+	+	+	+	+
56804	TB	1.806	+	1.586	+	+	+	+	+
150834	TB	2.662	+	2.468	-	-	-	-	-
38004	TB	2.443	-	1.722	+	-	-	-	-
68004	TB	2.871	-	2.375	+	-	-	-	-
98004	TB	3.691	-	0.971	-	-	-	-	-
107004	TB	0.875	-	0.732	-	-	-	-	-
92004	TB	1.632	-	1.394	-	-	-	-	-
97004	TB	1.491	-	1.979	-	-	-	-	-
118004	TB	3.182	+	3.045	+	+	+	+	+
173004	TB	3.643	-	3.578	-	-	-	-	-
173004	TB	3.232	-	2.916	-	-	-	-	-
374004	TB	3.896	-	3.718	-	-	-	-	-
376004	TB	3.243	-	2.56	-	-	-	-	-
282004	TB	1.249	-	1.234	-	-	-	-	-
283004	TB	1.375	-	1.17	-	-	-	-	-
308004	TB	3.708	-	3.353	-	-	-	-	-
314004	TB	1.863	-	1.399	-	-	-	-	-
317004	TB	1.162	-	0.972	-	-	-	-	-
312004	TB	1.709	-	1.453	-	-	-	-	-
380004	TB	0.238	-	0.461	-	-	-	-	-
451004	TB	0.18	-	0.2	-	-	-	-	-
478004	TB	0.188	-	0.468	-	-	-	-	-
419004	TB	0.384	-	2.392	-	-	-	-	-
411004	TB	0.306	-	0.874	-	-	-	-	-
421004	TB	0.287	-	1.456	-	-	-	-	-
3288004	TB	0.847	-	0.126	-	-	-	-	-
A6-87	Normal	0.098	-	0.063	-	-	-	-	-
A6-88	Normal	0.214	-	0.19	-	-	-	-	-
A6-89	Normal	0.248	-	0.128	-	-	-	-	-
A6-90	Normal	0.179	-	0.209	-	-	-	-	-
A6-91	Normal	0.115	-	0.151	-	-	-	-	-
A6-92	Normal	0.064	-	0.087	-	-	-	-	-
A6-93	Normal	0.072	-	0.058	-	-	-	-	-
A6-94	Normal	0.072	-	0.063	-	-	-	-	-
A6-95	Normal	0.125	-	0.159	-	-	-	-	-
A6-96	Normal	0.121	-	0.112	-	-	-	-	-
Cut-off		0.284		0.266					

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the construction of fusion proteins.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## CLAIMS

We claim:

1. A polypeptide comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:
  - (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu (SEQ ID NO: 115);
  - (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser (SEQ ID NO: 116);
  - (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg (SEQ ID NO: 17);
  - (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro (SEQ ID NO: 118);
  - (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val (SEQ ID NO: 119);
  - (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro (SEQ ID NO: 120);
  - (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser (SEQ ID NO: 121);
  - (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly (SEQ ID NO: 122);
  - (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn (SEQ ID NO: 123); and
  - (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID NO: 131)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID NO: 124) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID NO: 132), wherein Xaa may be any amino acid.

3. A polypeptide comprising an antigenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 1, 2, 4-10, 13-25, 52, 94 and 96 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an antigenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 196, 235, 237-242, 248-251, 290-293, 304, 311, 313-315, 317, 319, 323, 324, 328, 330, 332, 334 and 336, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 26-51, 133, 134, 158-178, 196, 235, 237-242, 248-251, 290-293, 304, 311, 313-315, 317, 319, 323, 324, 328, 330, 332, 334 and 336, or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4.

6. A recombinant expression vector comprising a DNA molecule according to claim 5.

7. A host cell transformed with an expression vector according to claim 6.

8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.

9. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with one or more polypeptides according to any of claims 1-4; and

(b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.

10. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with a polypeptide having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and

(b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.

11. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said

sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-153, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample the presence of antibodies that bind to at least one of the polypeptides, thereby detecting *M. tuberculosis* infection in the biological sample.

12. The method of any one of claims 9-11 wherein step (a) additionally comprises contacting the biological sample with a 38 kD *M. tuberculosis* antigen and step (b) additionally comprises detecting in the sample the presence of antibodies that bind to the 38 kD *M. tuberculosis* antigen.

13. The method of any one of claims 9-11 wherein the polypeptide(s) are bound to a solid support.

14. The method of claim 13 wherein the solid support comprises nitrocellulose, latex or a plastic material.

15. The method of any one of claims 9-11 wherein the biological sample is selected from the group consisting of whole blood, serum, plasma, saliva, cerebrospinal fluid and urine.

16. The method of claim 15 wherein the biological sample is whole blood or serum.

17. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA molecule according to claim 5; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

18. The method of claim 17, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule according to claim 5.

19. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

20. The method of claim 19, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

21. The method of claims 17 or 19 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

22. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA molecule according to claim 5; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

23. The method of claim 22 wherein the probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 5.

24. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

25. The method of claim 24 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

26. The method of claims 22 or 24 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

27. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide according to any one of claims 1-4; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

28. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

29. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

30. The method of any one of claims 27-29 wherein the binding agent is a monoclonal antibody.

31. The method of any one of claims 27-29 wherein the binding agent is a polyclonal antibody.

32. A diagnostic kit comprising:

- (a) one or more polypeptides according to any of claims 1-4; and
- (b) a detection reagent.

33. A diagnostic kit comprising:

- (a) one or more polypeptides having an N-terminal sequence selected from the group consisting of sequences provided in SEQ ID NO: 129 and 130; and
- (b) a detection reagent.

34. A diagnostic kit comprising:

- (a) one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337; and
- (b) a detection reagent.

35. The kit of any one of claims 32-34 wherein the polypeptide(s) are immobilized on a solid support.

36. The kit of claim 35 wherein the solid support comprises nitrocellulose, latex or a plastic material.

37. The kit of any one of claims 32-34 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

38. The kit of claim 37 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

39. The kit of claim 37 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin, dye particles and colloidal particles.

40. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule according to claim 5.

41. A diagnostic kit according to claim 40, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA molecule according to claim 5.

42. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the primers being specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

43. A diagnostic kit according to claim 42, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

44. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA molecule according to claim 5.

45. A kit according to claim 44, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 5.

46. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

47. A kit according to claim 46, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS: 3, 11, 12, 135, 136, 151-155, 184-188, 194-195, 198, 210-220, 232, 234, 256-271, 287, 288, 298-303, 305-310, 312, 316, 318, 320-322, 325-327, 329, 331, 333, 335 and 337.

48. A monoclonal antibody that binds to a polypeptide according to any of claims 1-4.

49. A polyclonal antibody that binds to a polypeptide according to any of claims 1-4.

50. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.

51. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6 (SEQ ID NO: 99).

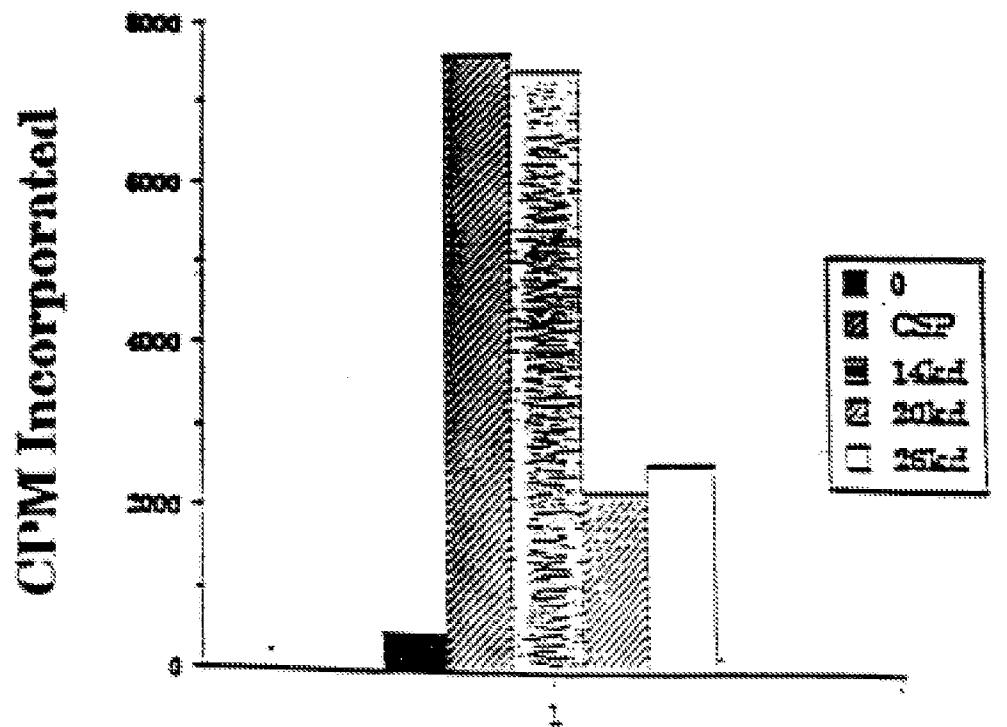
52. A fusion protein comprising a polypeptide having an N-terminal sequence selected from the group of sequences provided in SEQ ID NOS: 129 and 130.

53. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO: 150).

54. A diagnostic kit comprising:

- (a) one or more fusion proteins according to any one of claims 50-53; and
- (b) a detection reagent.

## D7 T Cell Proliferation



## D7 IFN<sub>γ</sub>

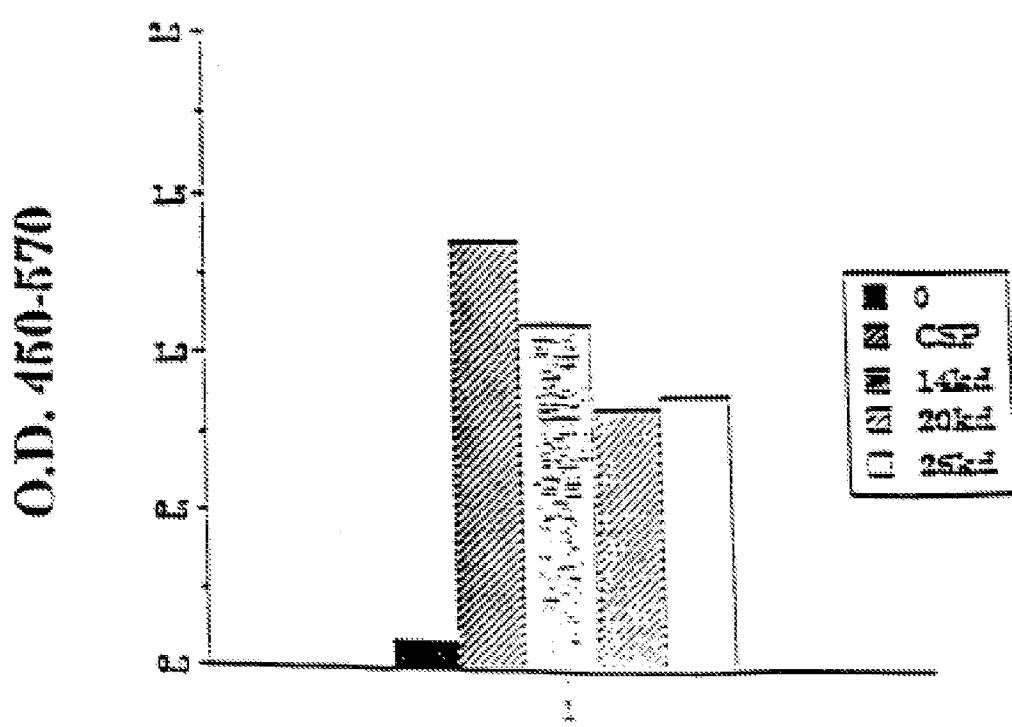
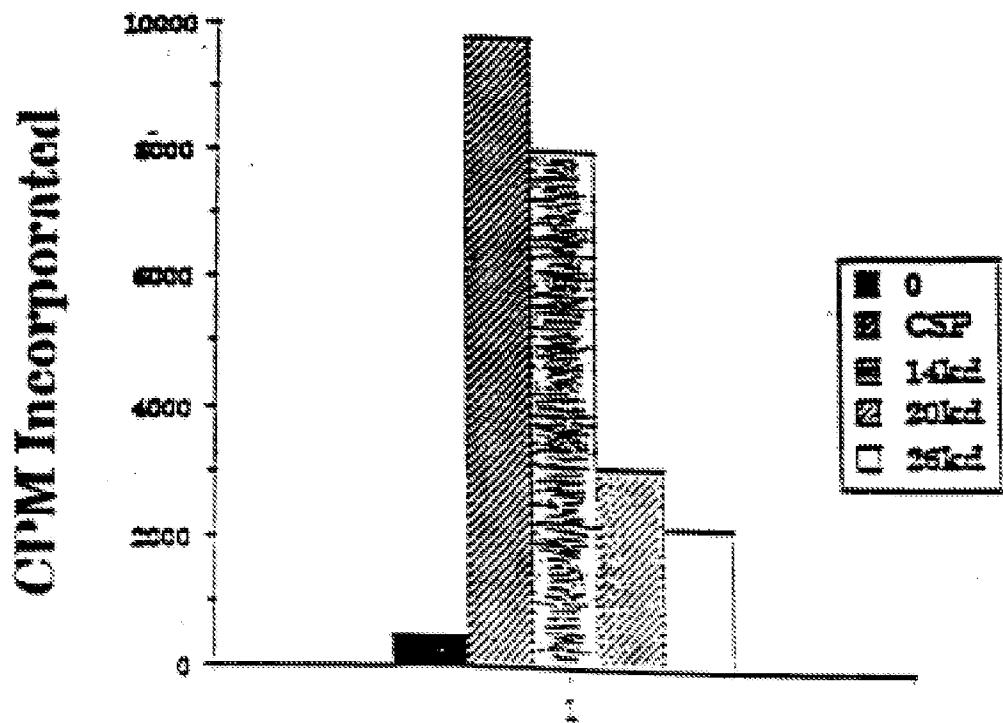


FIG. 14

## D160 T Cell Proliferation



## D160 IFNg

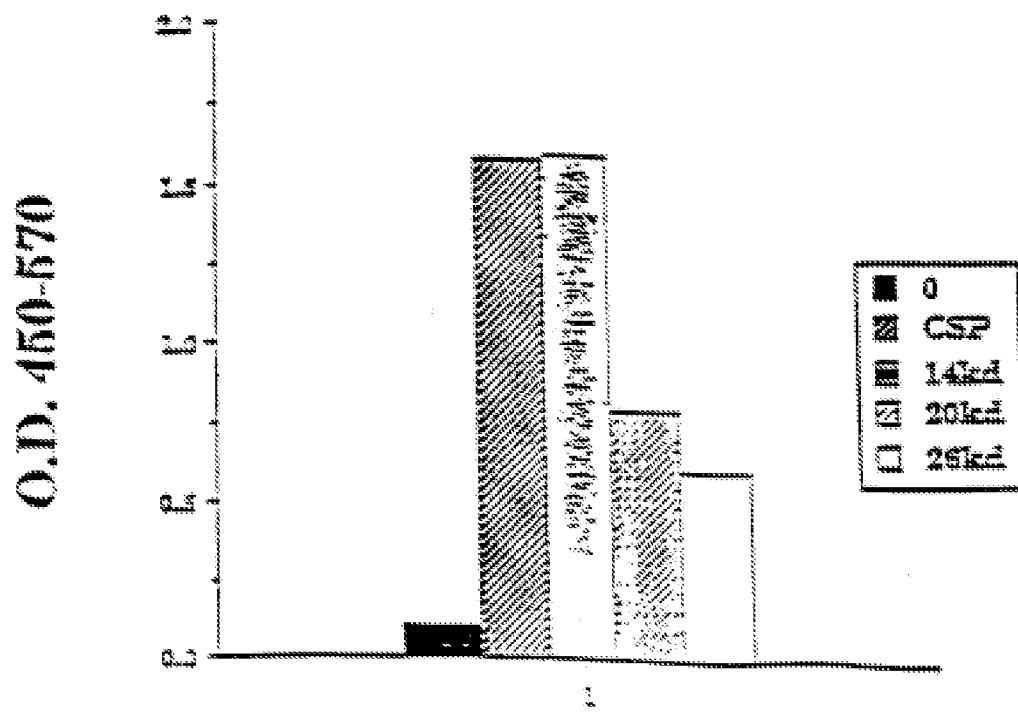


FIG. 1a

2A

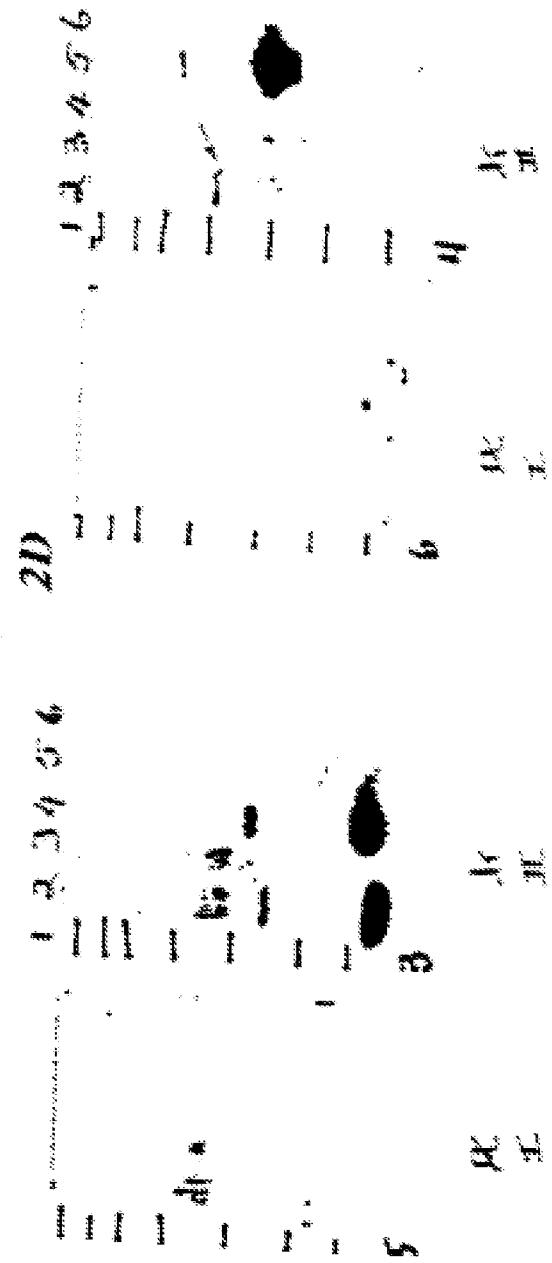


2B



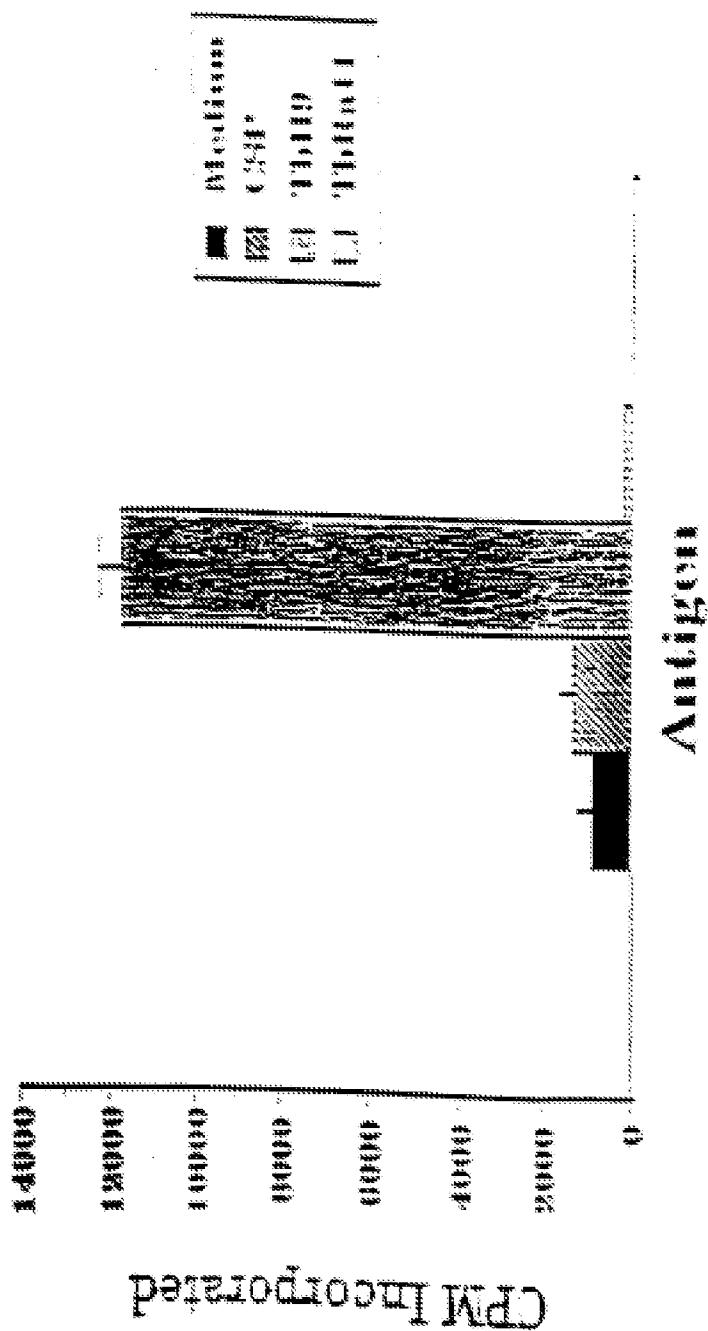
143456

2C

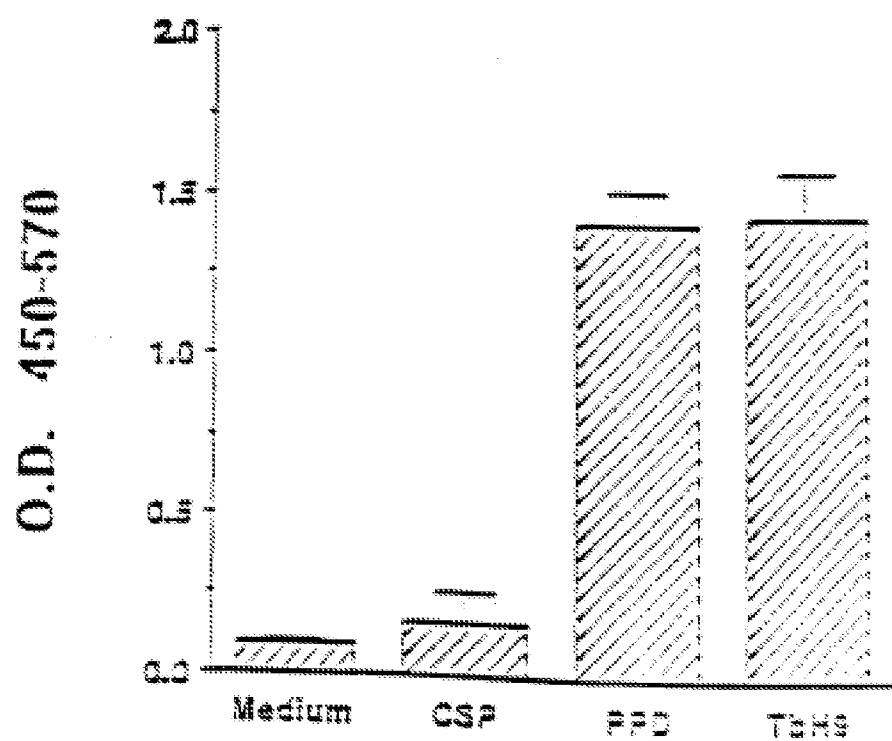


FIGS. 2A-2D

**T**cell clone 131T<sub>0</sub>H9  
responds poorly to CSF



1153

**T Cell Clone PPD 800-10 IFN $\gamma$  Production****FIG. 3B**

10000  
8000  
6000  
4000  
2000  
0

0.000  
0.005  
0.010  
0.015  
0.020  
0.025  
0.030  
0.035

0.000 0.005 0.010 0.015 0.020 0.025 0.030 0.035 0.040 0.045 0.050 0.055 0.060 0.065 0.070 0.075 0.080 0.085 0.090 0.095 0.100

FIG. 4

Initial  
Freeze/thaw

1st freeze

2nd freeze

3rd freeze

4th freeze

5th freeze

6th freeze

7th freeze

8th freeze

9th freeze

10th freeze

11th freeze

12th freeze

13th freeze

14th freeze

15th freeze

16th freeze

17th freeze

18th freeze

19th freeze

20th freeze

21st freeze

22nd freeze

23rd freeze

24th freeze

25th freeze

26th freeze

27th freeze

28th freeze

29th freeze

30th freeze

31st freeze

32nd freeze

33rd freeze

34th freeze

35th freeze

36th freeze

37th freeze

38th freeze

39th freeze

40th freeze

41st freeze

42nd freeze

43rd freeze

44th freeze

45th freeze

46th freeze

47th freeze

48th freeze

49th freeze

50th freeze

51st freeze

52nd freeze

53rd freeze

54th freeze

55th freeze

56th freeze

57th freeze

58th freeze

59th freeze

60th freeze

61st freeze

62nd freeze

63rd freeze

64th freeze

65th freeze

66th freeze

67th freeze

68th freeze

69th freeze

70th freeze

71st freeze

72nd freeze

73rd freeze

74th freeze

75th freeze

76th freeze

77th freeze

78th freeze

79th freeze

80th freeze

81st freeze

82nd freeze

83rd freeze

84th freeze

85th freeze

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89th freeze

90th freeze

91st freeze

92nd freeze

93rd freeze

94th freeze

95th freeze

96th freeze

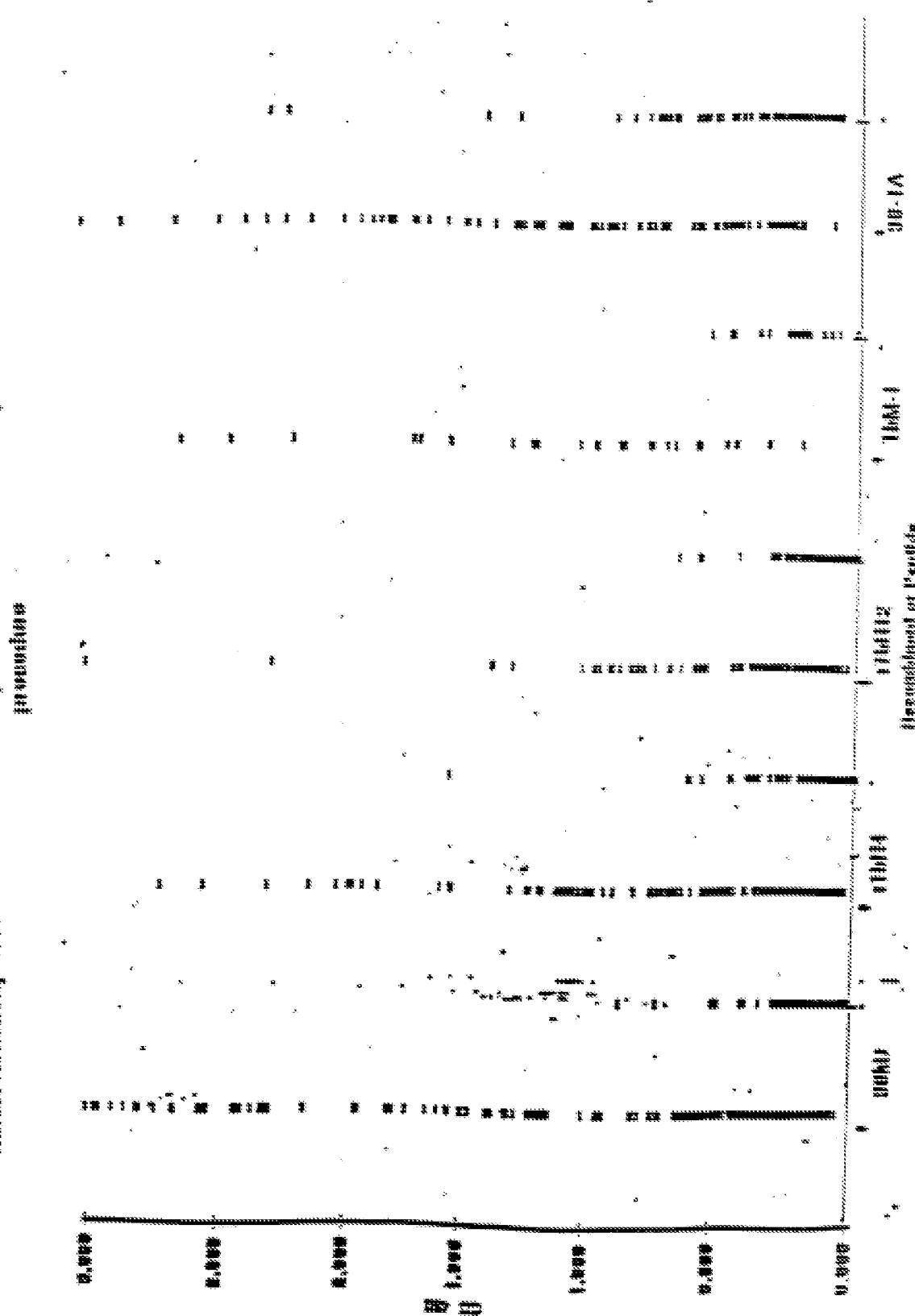
97th freeze

98th freeze

99th freeze

100th freeze

**FIGURE 1: INFLUENCE OF INVESTMENT PER UNIT OF CAPACITY AND OF INVESTMENT PER CAPACITY ON INVESTMENT**



## FIG. 6

Immunity of leucokinase against *Mycobacterium tuberculosis* infected mice to *M. tuberculosis* irradiation,  
with or without immunotherapy

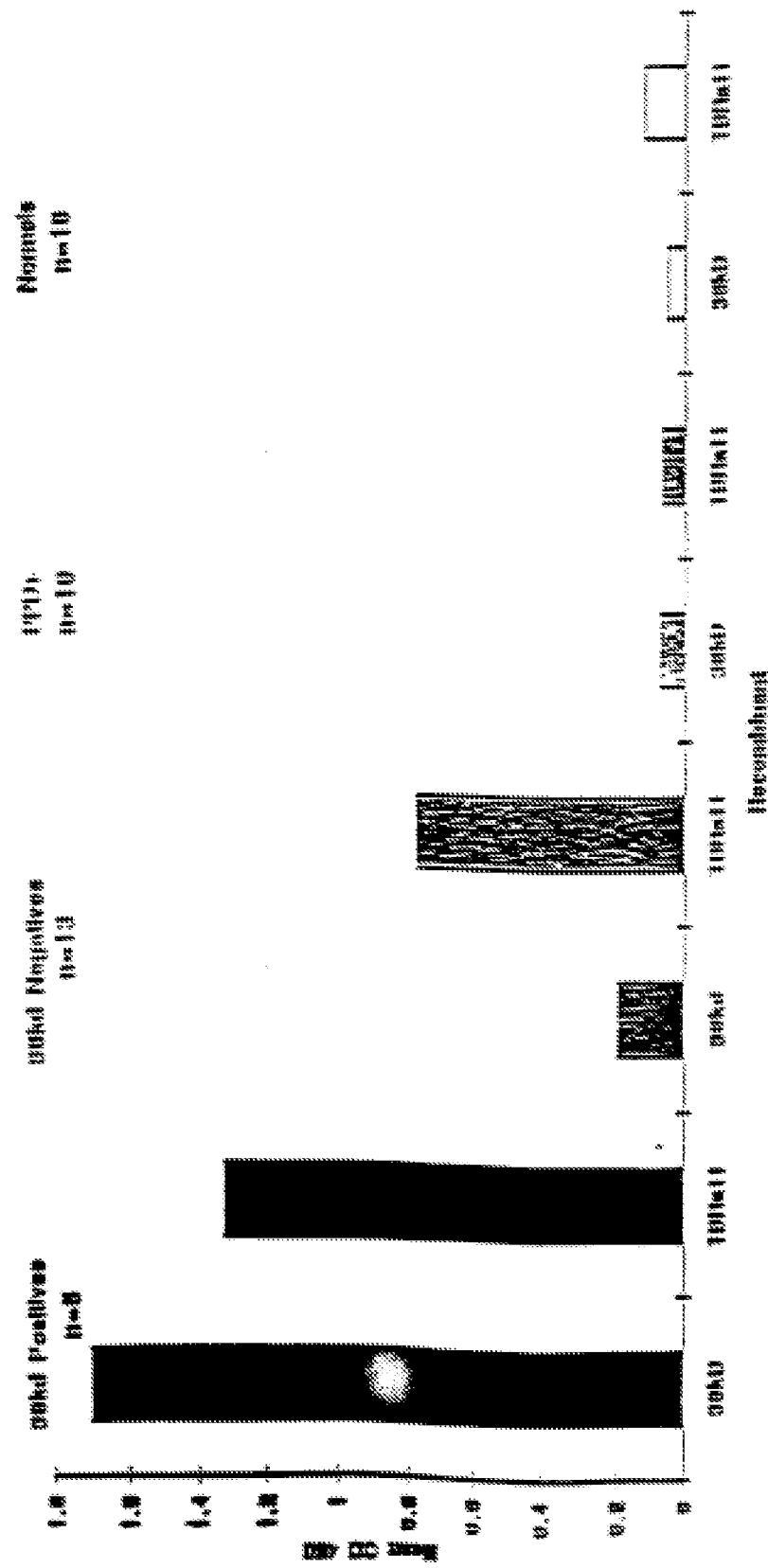
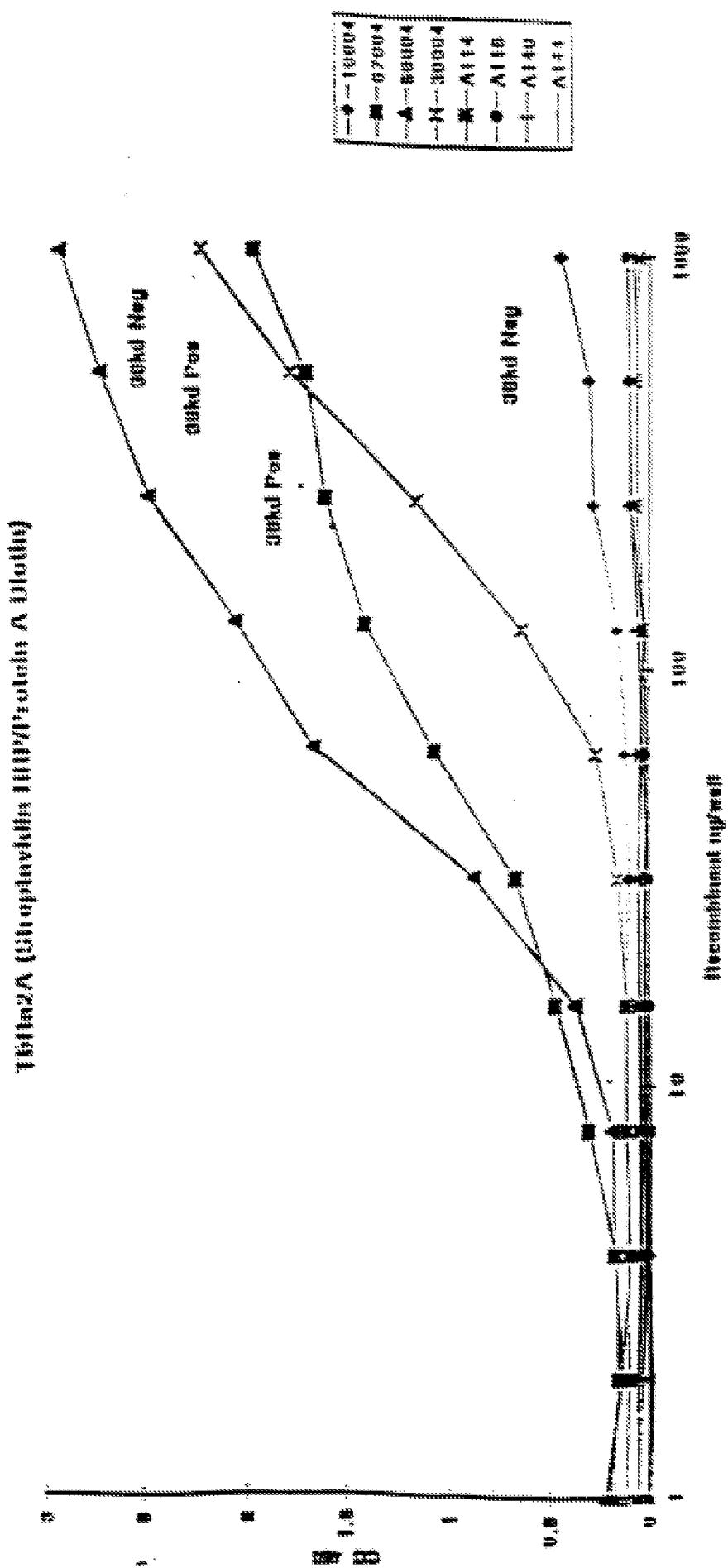
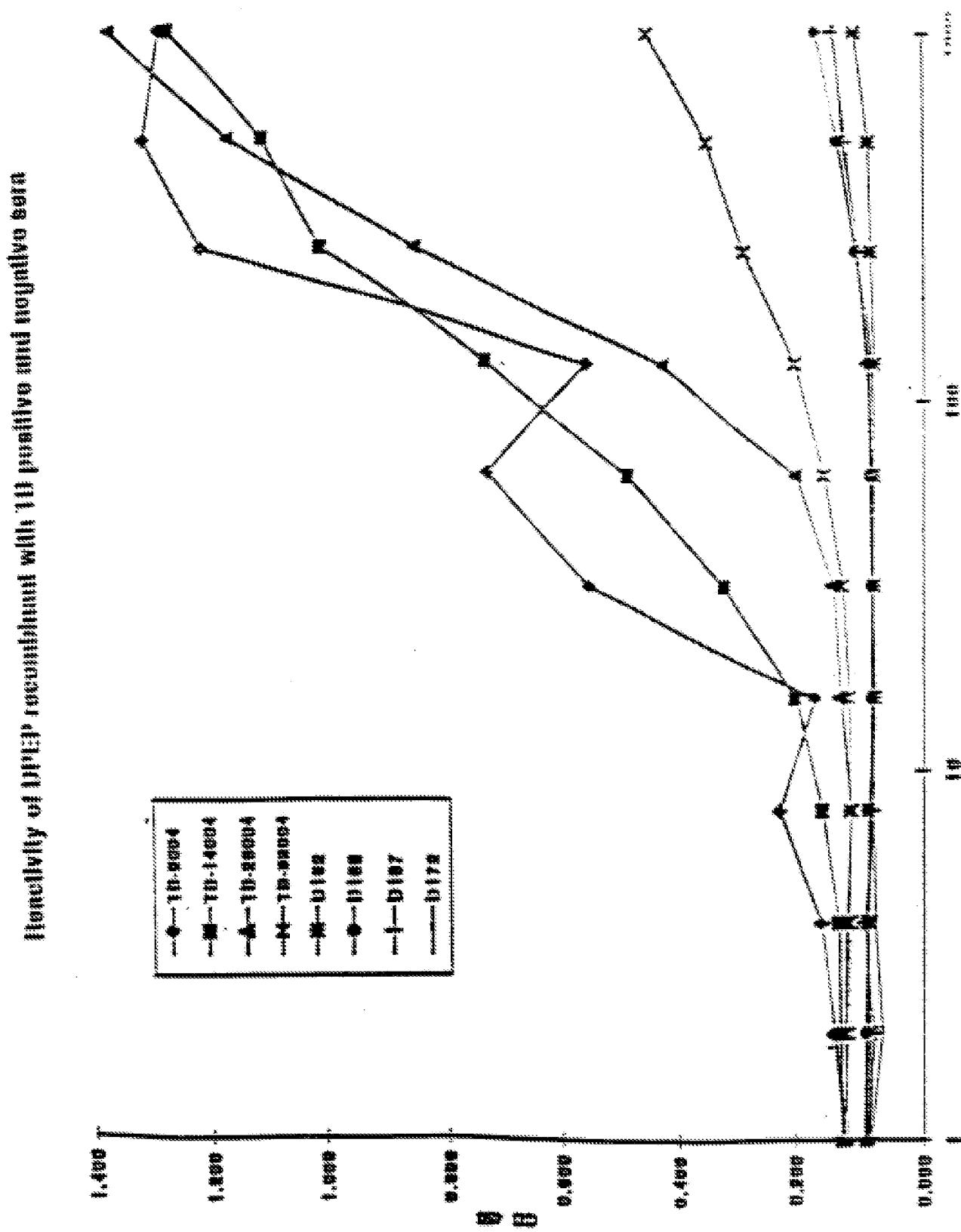
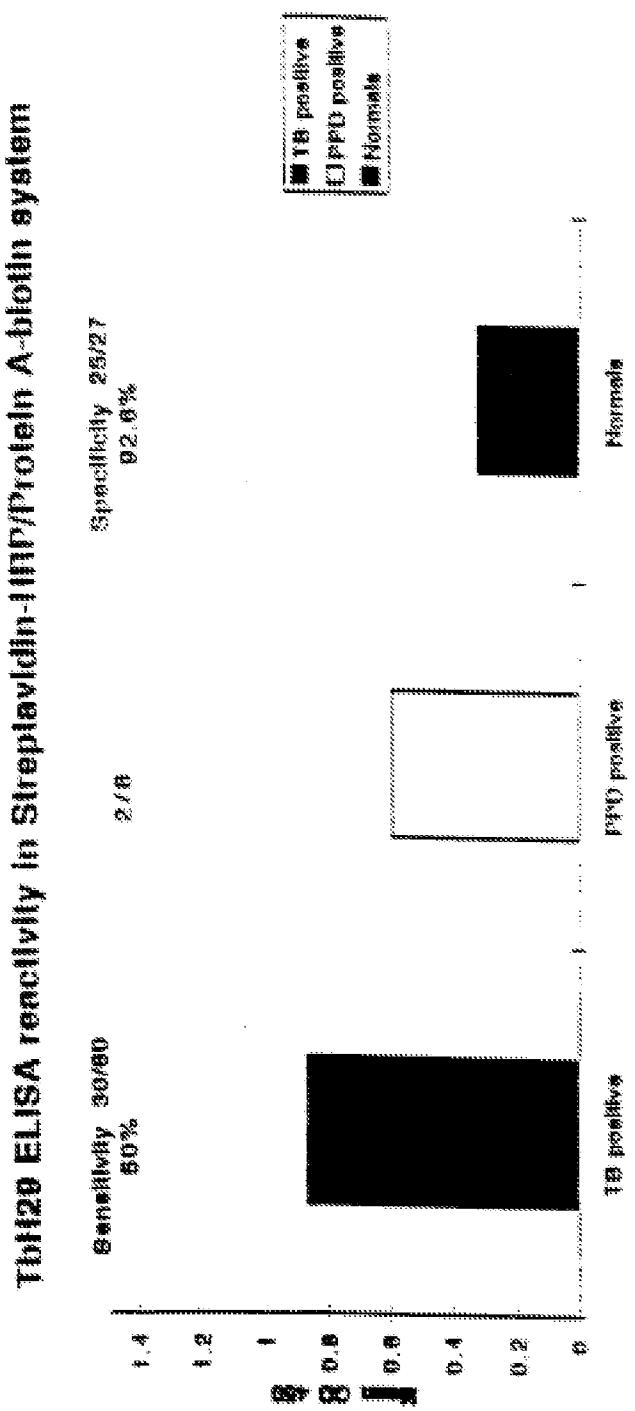


FIG. 7





116



## Th1133 ELISA reactivity

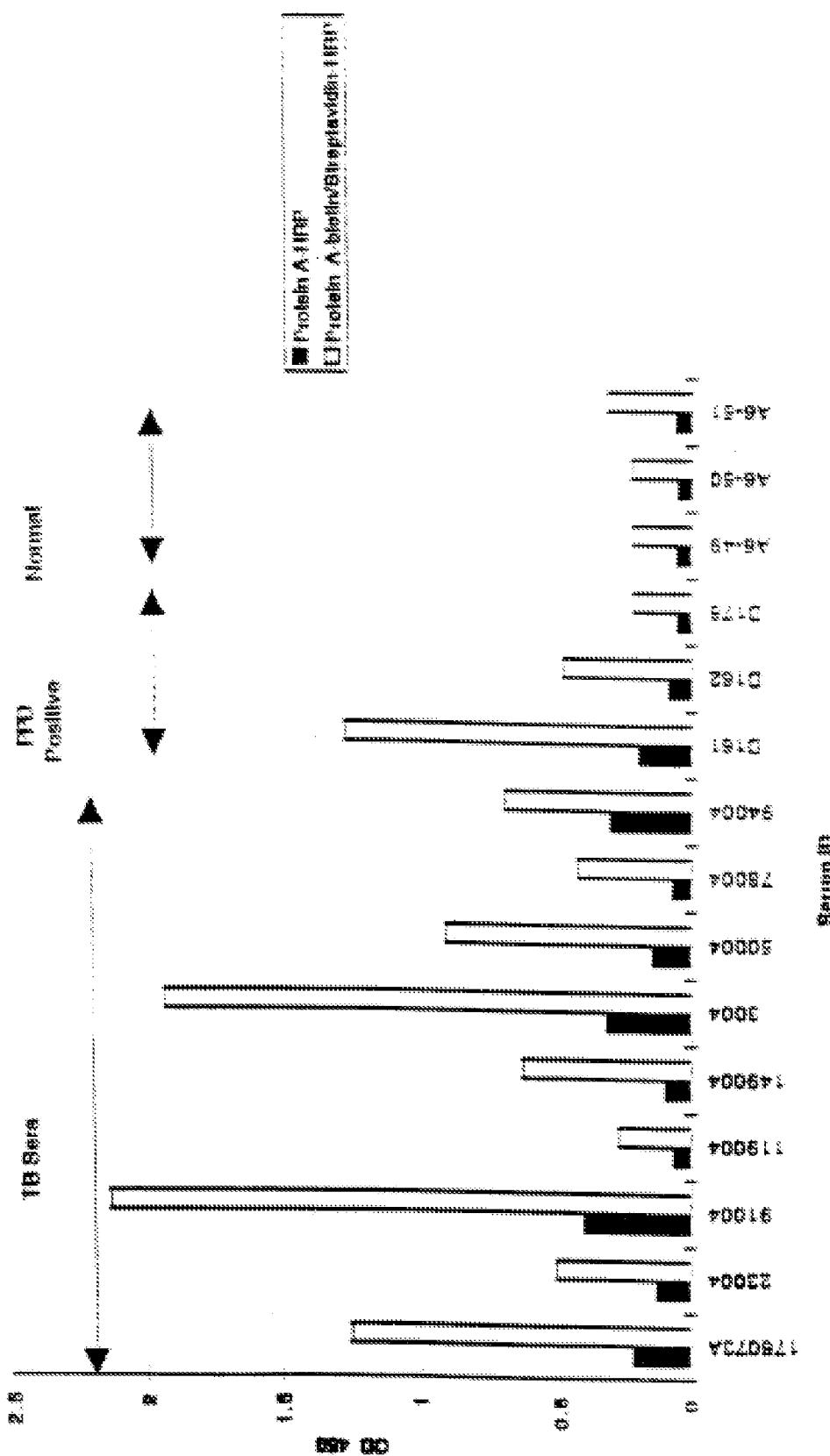
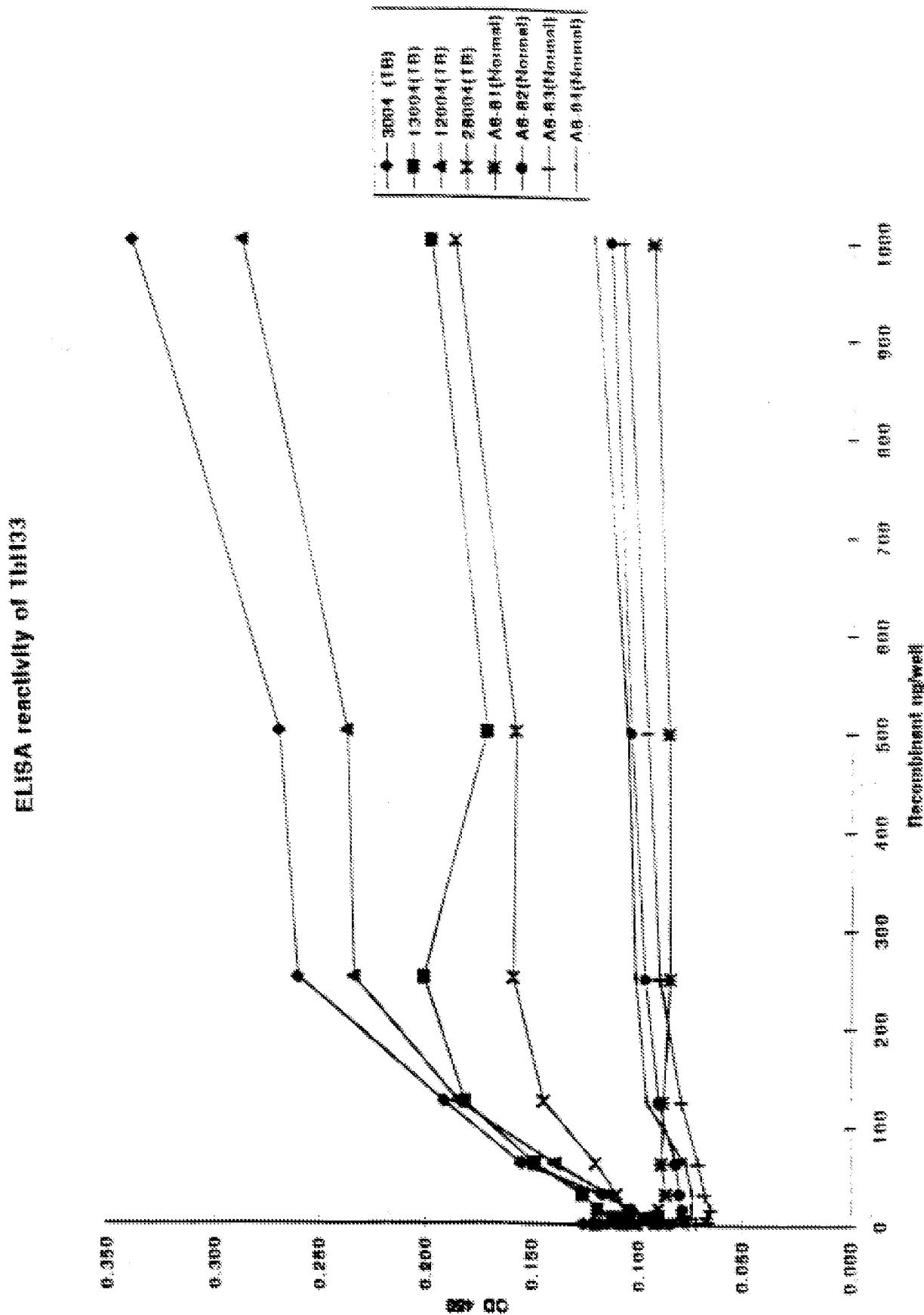
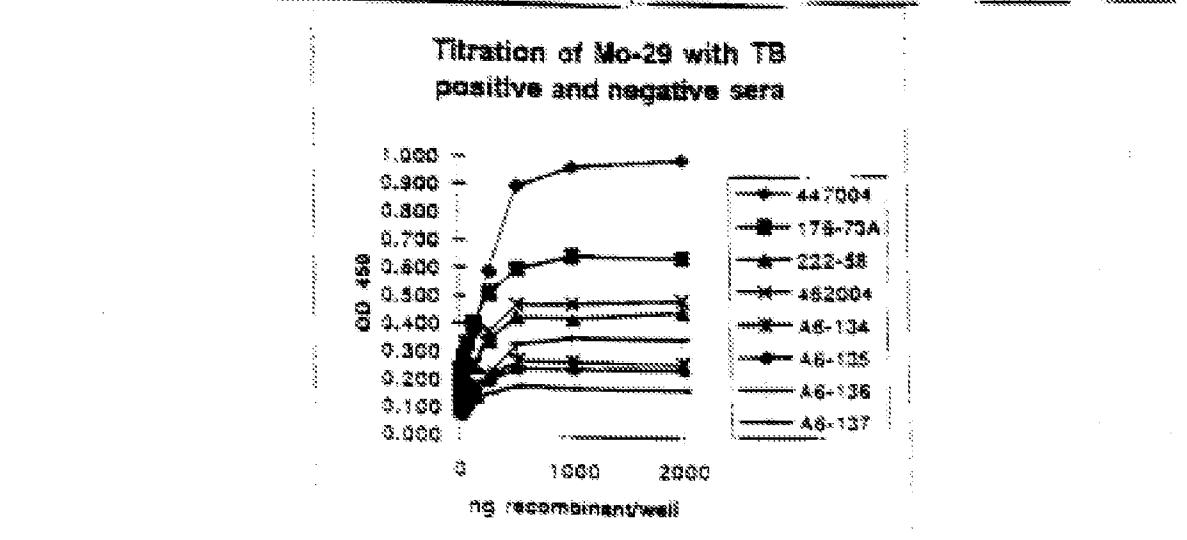
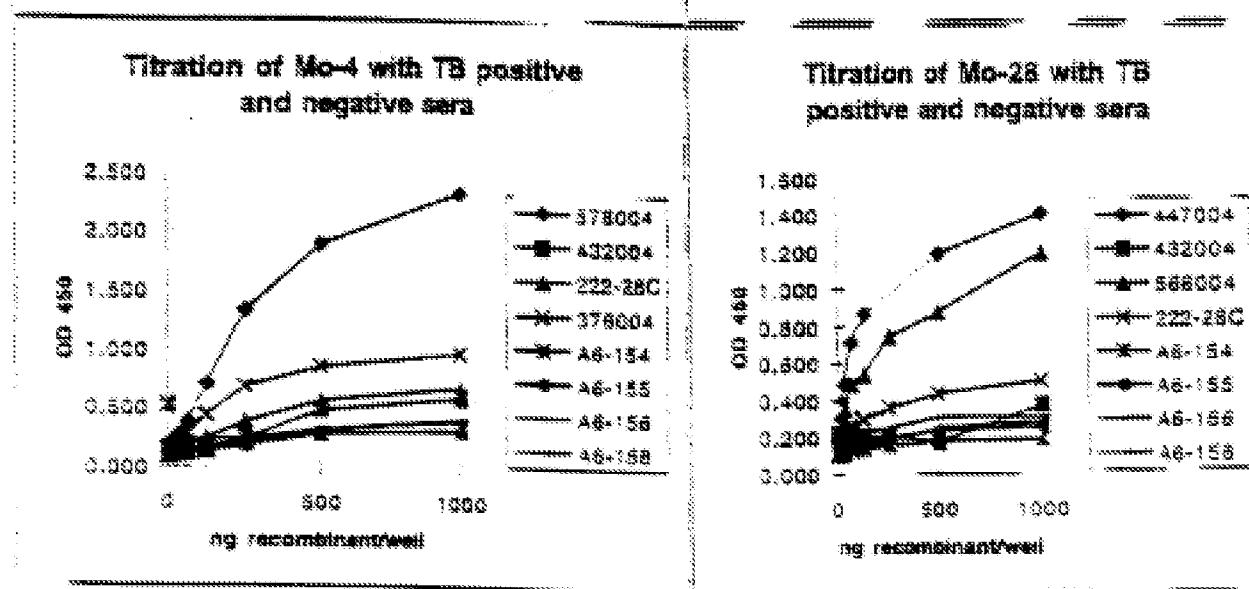
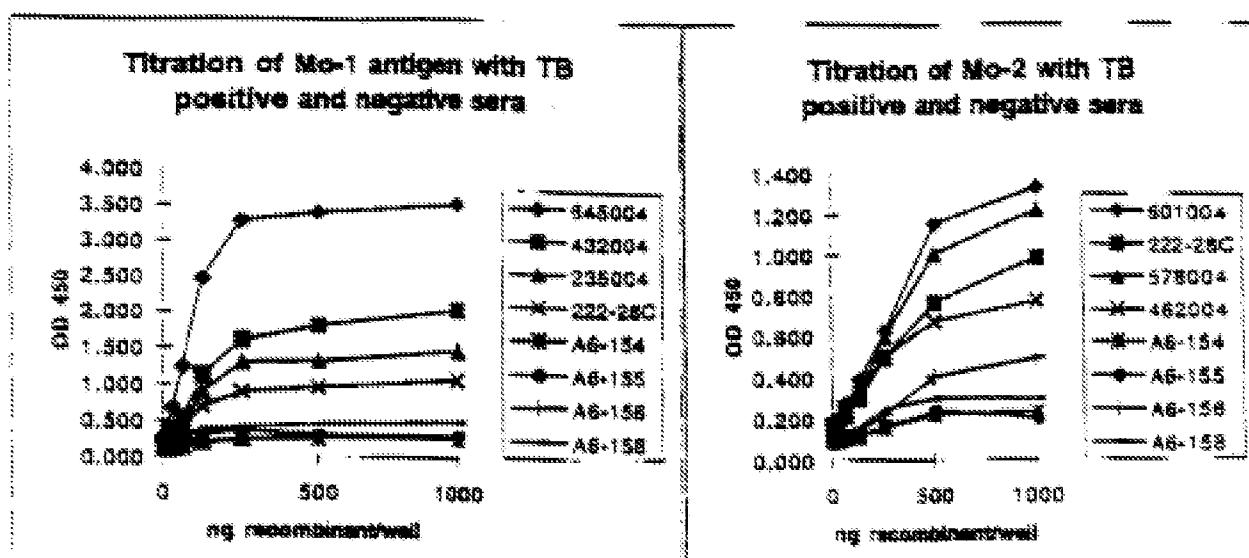


FIG. 10





## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Reed, Steven G.  
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Lodes, Michael J.  
Hendrickson, Ronald

(ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS

(iii) NUMBER OF SEQUENCES: 380

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEDD and BERRY LLP  
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue  
(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: USA  
(F) ZIP: 98104-3092

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 08-MAY-1998  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,192  
(C) REFERENCE/DOCKET NUMBER: 210121.417CS

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4968  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAAGCACCC	GTACTTTGAA	CCAAACGCCAC	AATGGACCGG	CAAACGCCAC	GAAGAACACA	60
ACCATCAAGA	TGCTGAAATC	GTGTCGCCCA	GGTCTGACCG	CCGGCGCTGC	AATGGCCCGC	120
CTTGCGCCCG	GTGTGACTTC	GTGTCGGT	GGGGGGCCCG	TGTTATACCA	GTGTCGCCCG	180
GTGCTTTCG	GGGGCGCACT	GGCTTTCAC	GGGGATCCG	CCCCTGACGT	GGGGACCCCG	240
GGCCAGTTGA	CGAGCTCTCT	CAACCGCTTC	GGCGATCCCA	ACCTTGTTTT	TGCGAACLAC	300
GGCGACTTTC	TGAGGAGCGG	GTGGGGGGGC	ACCGACCCCG	GGTGGGCTCA	CCACAAGCTG	360
AAGAAGGCGG	CCAGAACCGG	GGATCTTCCG	CTGTTCTTC	GGCTGGAA	GTGCGACCGG	420
GGGGCGCCCG	GTTCGGCCAC	GGGGCGCTTT	TGTTCTTCCG	GGCTGGACGT	GTGGTCCCGG	480
GTGACCGAGA	ACGTCACTTT	CGTGAATCAA	GGGGCTGAA	TGTTTACCG	GGGATGGCGG	540
ATGGACTTTC	TGCGGGCGTC	AGGGAACTTC	ATGGGGGGCC	GGGGTTAGC	GGGGTTTTCG	600
GGTACCGCGC	GGGGCGCTTG	ACGGCTCCAT	GTGGAAACAT	GGGGCTTTTA	GGGGCTTCTC	660
GTGTCGGCG	GGGGGGCGCG	ACGGGGCGGT	CCAAACCGTC	GTGGAGATTC	GTGGTCTTCG	720
GGGACCGAGC	AGACGGGGCG	GGGGGGCGGT	CCAAACCGTC	GTGGAGATTC	GTGGTCTTCG	780

## (xii) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCACTTAC	ATGACCACTA	GTATGAAATC	ACCGTAGAGA	GGACCTTGGT	GTTCGGCGCA	60
GACTTCTTCA	GGAGGCTGAA	GGCTCTTCCG	CAAGGCGTAA	GGAGGACCGC	GGGGTGGCGG	120
GTGGAAAGGGC	TGCGGGCGGG	GTGGCGCTTT	CTGGTACTCA	AACCGACCCG	CAACGGCGCG	180
TCGGCGTTTC	TACGTGACCA	ACCCATGAGG	TGGCTGGTC	GGCATCCCGA	GGGGACACAA	240
TTTCTGACGG	ACGTGGCGT	GGGGCGTGGC	GTGGTGAAT	TCCGGTGGAA	AAACAAACAA	300
TTGCAATGCG	TGATGTCGG	GGGTGTCAC	GGGACCTTAC	TCAACGGCGA	GGGGCGTGGAT	360
TTGGCGCTGC	TGGGAACCGG	GGACGGGGTC	GGGTGGCGCA	ACGGGGGTT	GTGTTCTTGG	420
ACCGGACCGA	ACGGGGGGCA	GGTGGCGCG	GGTACCGGGG	GGGGTGGCGA	GGGGGGCGCA	480

CCCCCGCTT CCCCCGATG TGTATTCGG CGCTTCTGG AGCTTGCTG AGCTGATTG	540
CCCTGATTC CACCATGTCG AAGATTGAT TCTTGCGAGC CTTCAGGTC NCGCTTAACC	560
CCCCCGGGC CTGATTCGG CGTTTGGCG CGTTCACTG CTAACTGACT CGCGCGCG	580
TTCGAATTC TTCTTCGCT CGCCGAAAG CGACGTTAA CTTCGCGCTG CGAAGCTGA	710
TGCGGGGGG TTGCTGAAAG CGCCATTCGG AT	753

(2) INFORMATION FOR SPC IN NO. 1.

46 | PRODUCTS | [enr.com/resources/special/](http://www.enr.com/resources/special/)

- (A) LENGTH: 613 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANGENESS: single
  - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1

CATATGCGATC	ACCCGTCAACCA	TCTGACTTCTT	AACGCCCGAG	CGCGTGCGGG	CGCTTGCGCA	600
CCACCGCGCA	CGCGGCGCGA	TGCGTGTGCT	ACCTTCGATC	TGTTGCGCA	TGCGTGTGCG	660
CAGCGCGATG	CGCTATGTTT	GTCUTGACT	CGAGATCGGC	CGCAATCGAA	TTCGCCGCGT	720
CGCGCGCGCA	CGCTCGGAA	GTCTTGCGG	ACCGATTTTG	AAGTCGCCGT	CGAGATTC	780
ATGCTGCTCA	CGCGTGTGCT	TTGGCTGT	TGTTGCCGTC	TGCGCGCGTC	CGCGCGCGCA	840
ACCTATCGAT	AGGAGTCAA	AGGACCGAT	ACCGGCCAG	CGTGCGCAT	TGAATGTC	900
CGCCCGCGT	AGAACATCGA	CGTCGATTC	CGAGCTTAC	ACCGCGACCA	GAAGTCGTC	960
GAATAATTCA	TGCGCGAC	CGCGGAGAG	TTCCTGCGG	CGCGCACATC	GTCGACTCG	1020
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1080
CGTGTGACCG	ACGCGCTGT	GCTCAGGTC	TGACCGACG	CGCGCGCGAC	CGACCGACCG	1140
ACCGCTTACA	ACGCGTTACA	TTGCGGACCG	CGCTATCGCA	ACCGATCGAC	CGTGTGACCG	1200
CGACCGTACA	ACGCGTTACA	TTGCGGACCG	CGCTATCGCA	ACCGATCGAC	CGTGTGACCG	1260
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1320
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1380
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1440
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1500
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1560
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1620
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1680
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1740
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1800
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1860
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1920
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	1980
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2040
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2100
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2160
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2220
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2280
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2340
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2400
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2460
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2520
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2580
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2640
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2700
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2760
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2820
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2880
CGCGGAGCGG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	2940
CGTGTGACCG	CGTACGATT	GAATATCGAC	TGCGCGCAT	ACCGATCGC	GAATCGCGG	3000

(3) INFORMATION FOR 820 IN NOTE 1

#### (4) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 4:

CGGTATTAAC ACAGGCGCTT CGGATTAATT CGAGCTTCCC CAGGGTGCCC AGCGATTCCC	60
CATTCGAGTC GGGCAAGCCA TGGCAATGCC CGGGCAGATC CGATCGCTG GGGGTAACTC	120
CACCGTTCAT ATCGGGCTTA CGCGTTTCTT CGGCTTGGT GTTGTGACA ACGACGGAA	180
CGCGCAAGA GTCCGAACCC TGGCGGGAG CGTTCGGCG CGAGCTTCCC CGATCTCCAC	240
CGCGCACCTG ATCACCGCC TGGACGGCC CGGATCAAC TCGGGCGACG CGATGGCTGA	300
CGCGCTTAAAC CGCGTCAAC CGCGTTCCT CGTGTGCTG AACTGGCAA CGAATCGCC	360
CGCGACGCT ACAGGGAAACG TGACATTGGC CGAGGACCC CGCGCTTAT TTGCTTGGCG	420
ATACCGACCC CGAGGCGCC AATTGGA	447

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 5:

CTCCGACTGC CGTCGGGAG TATTCGGGCC AGCAATGTC TGGCGACCC CGAACGGAT	60
CGCGTTCCTCC CGCGTGGCG CGTGTGAAAC CGCGCGCCGC CGAATGATCG CGTGTGCTT	120
AGCGCGCGAA CGCGGAGCC CGAAATGCC CGAGTGGAA CGCGCGAAAT TTGGCGGGCC	180
CGCGCGACCG CGAGCTGGCG AATGGCGCGA CGGAGGAGT CGCGCTTAT CGCGAGCTG	240
ATCGAAATCAA CCTGGATTCG CGCTGGGGG CGATTTGACA ATCGAGCTAC TGAGCGAAA	300
TGAAATGATG AAAAGGGGG CGAGCTCCG ATGTTCTGTG CGTGTAGGT CGCTGCTCG	360
CGTGGCGGT ATCGAGATGT TCTTCGCGA AAAGCTGATCG CGAGGAACAG CGTGTGCG	420
CGAAGGCGAA CGGTGCGAA CGCGGCTTCC CGCGGAAATG CGAAGAGCGA TTGGATGCGA	480
CGAAGGCGTG CGACGAGGAA AATGCGGGG CGAAGGAAAC CGAAGGAGGG CGTGTGCTTG	540
CGTGTGCTTG CGTGTGCTTG CGTGTGCTTG CGTGTGCTTG CGTGTGCTTG CGTGTGCTTG	600
CGTGTGCTTG	

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCGATGCG AACCACCTCA CTAAACGGAA CAAAAGCTTG AGCTTGCACCG CGGTGCGCGC	60
CGCTCTTGAA CTAGTCGATM TTTCGCGCTG CAGGAACTTG GYACGACGAT TGGACGACTG	120
TAACGCTCTT GTTACGCTGA TCAAATGACC GACGACATCC TGTGATCGA CGGTGCGAA	180
CGGTGCGAA CGGTGCGCTT AAACGCGCC CGTGCCTTA AGGGCGCTTC CGGGCGCTTA	240
CGGGCGCTTA TTTCGCGSY GTTCGCGAC CGCGACGCG AGGACGACAT CGCGCGCTG	300
AGGACGACG AGGACGACG CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	360
CGGGCGCTTA CGGGCGCTTA TGTGACGGCG CGGGCGCTTA ATGGACGACG CGGGCGCTTA	420
CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	480
GATGGCGCTT GAGGACGCG CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	540
CGGGCGCTTA AGTGTGCGT TGGACGCGAA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	600
CGGGCGCTTA GACTACCTT CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	660

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC CGGGCGCTTA AGGGCGCTTA AAACGGCGATC GACGGCGCGC TGGCGAGCT	60
CGGGCGCTTA CGGGCGCTTA TGGAAATCATG AAATTTCATC ACCATATTGA CGCTCTGGCG	120
CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	180
CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	240
CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	300
CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	360
CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	420
CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA CGGGCGCTTA	480

CCGCGCGCGC CGTTCGGCC CGATGTGGCC GCGGATAACC TGGCGACGCC CGTGCAATTG	540
GACTTCATGG CAGCTTGTGT CCTGGCTGTT CTGGACCAA CGTCTCTGCC CGCGCGCGCG	560
CGCGCCGAAC AGCTCATGCC CGCGCGCGT CGACTGTGT TCGCGCGCAA CGTGCAGCG	580
CGACATGCC CGCGCGCGT CGCGCGCG CGTGGCGCG CGTGGCGCG CGACGCTGCC CGACGATCTG	600
CGATGGCAA CGCGCGCGA CGCCATGCC AGCGCGCG CGCGCGCG CGACGATCTG	620
CGACATGCC CGCGCGCGT CGCGCGCG CGTGGCGCG CGACGCTGCC CGACGATCTG	640
TGGCGCGCG AGCCAATGCC GATGAGACT CGCTGACAA ACCGGACAC CGCGCGCG	660
CGCGCGCG CGCGCGCGT CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	680
CGTACCGACG AGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	700
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	720
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	740
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	760
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	780
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	800
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	820
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	840
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	860
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	880
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	900
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	920
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	940
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	960
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	980
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1000
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1020
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1040
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1060
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1080
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1100
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1120
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1140
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1160
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1180
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1200
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1220
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1240
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1260
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1280
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1300
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1320
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1340
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	1360

## (ii) INFORMATION FOR SEQ ID NO:8:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGACGACCC CGATATGCC CGACCGCG CGACGCGCG CGCGACGCC CGCGCGCG	60
CGATCGCTCC CGTGGCGCG ATTCAAGACT CGCTGGCGCG CGCGCGCG CGCGCGCG	120
TGATGACGT CGCGCGCGT TACATCGCTT ACCGGCGCG CGCGCGCG CGCGCGCG	180
CGTAAAGCGT CGTGGCGCGT CGGACGACT TAAAGCTAG CGTGGCGCG CGCGCGCG	240
CGCGCGCGT CGTGGCGCG CGGACGACT CGTGGCGCG CGCGCGCG CGCGCGCG	300
TGATGACGT ATCGCGCG CGTGGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	360
CGCGCGCGT CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	420
CGCGCGCGT CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	480

CGATTTACCA TTGGCTTCAA TCGATTTTC CGAACCTTGC ACAGGGCTCC GAACTTGCCC	540
GGGCTTGGC CGGACCCCGA TATGGTTCA GGCACCTTCC ACCGGGGGGG GATGGGGGG	560
CGTGGGGG CGGGCGGT AGGGGACCG TTTGGTTTCT AGGGGTTGTT GACGGGCG	580
CGGGTGTG CTGGATGGCC CGTGGGGGTC TATGGCTGTC GTTGTATGTC	600
CGGACCCGA TATCTGTGAT TTGGCTACCG CGAGGGCGA ATCCCCCGCC GAGCTTGGC	620
ATTTCACCT ATGGCTTGT GTGGACCCGC CGTGGGGGCG CGGGCGGT CGGGCGGT	640
TACGGGGT GTGGATGCC CGAACCCGA AGGGGACCG CGGGATCCCG CGGGGGGGC	660
TGTTGACGC CATGGCGAA CGGGGGCG CGGGGGCG TGGGGGGGCT GTTGTGGC	680
ACGGGATCA TGGGGGAA CGGGGGCG CGAGGGCGT CGGGGGGGCG ACCGGGCGT	700
CGGGGGGGT CGGGGGGGT CGTGGGGT CAGTAACTG CGGGGGGGT AACGGGGGGC	720
CGGGGGGGT CGGGGGGGT CGTGGGGT CAGTAACTG CGGGGGGGT AACGGGGGGC	740
TGGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	760
TGGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	780
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	800
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	820
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	840
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	860
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	880
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	900
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	920
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	940
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	960
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	980
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1000
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1020
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1040
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1060
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1080
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1100
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1120
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1140
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1160
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1180
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1200
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1220
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1240
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1260
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1280
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1300
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1320
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1340
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1360
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1380
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1400
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1420
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1440
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1460
CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGC	1480

## (ii) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAAT CGTGGCTGGAT CTGGAACTCC GTGGGCCCCGCT ACCTTACGGAG ATCTACTGGC	60
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG TGGTGTACT CGGGGGGGGG GTGGGGGGGG	80
TCAATGGGGCTT CGGGGGACAGC AGGGGGGGGTG CGAAACGGGT CGGGGGGGGG ACAGGGGGGT	100
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	120
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	140
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	160
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	180
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	200
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	220
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	240
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	260

CCCGGGTCCA CGGCGGCCG GTCGTCAAGG AACGGTGACGA TTGCCCCCAT TGTACCTTG	360
CGATGAAAGG TTTCGACGAC GCGCGCGCTG AGTACTTGCG CGACCGCGG AAGTTTACCA	420
TGCTGGTCAC CAACTATTCG CTGGGGTCTT GTAAACCGA CCTTGGGCC CGGGTGTTCG	480
CGCTTACGT TTACTTGCTG CAAACACAGC GGTGTTGGTC CAACCTGGAC TGCTGGCGCT	540
CGATGAGAC CGTGTGAG ACCTTTTCAC CGGGTACCA CCTAACGACC CGGTGACCT	600
CGACCGAT CGATGCGG CGCGCTGC CATTGGCCG CGCGCGAT CGCGCGCGCA	660
CCTACAAATCT CGTGTACAA CTGGGGATC TGCGCTGCT CGCGCGCG CGCGCGCG	720
ATCAGCGCC CGCGCGCCC CGCGCGTAC CGCGCGCG CGCGCGCG CGCGCGCG	780
CGGACTTGC CGCGCGAGG CGATAATTAT TGATCGTGA TTGTCGATTC CGCGCGCG	840
GACGACCGT CGCGCGCG CG	862

## (3) INFORMATION FOR SEQ ID NO:10:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (2) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCGCA CGCGCGAGG GTCACATGCC TCGCTGGCTG TCGACGGAC CAATGAA	60
GACACCGCCG CGCGCGAT CGTGTAACTA CTGGGGCTG CGCTGGCGC CGACCGTCA	120
CTGGGGAGG CGCGCGCTG CAACTGGTC CGACCGCCG CGATGACAG CGCGCGCG	180
TTGGTGGCG CGCGCGCTG CGAAGCGCC CGCGCGCG CGGGCTTAAC TTTCGAGCT	240
CGCGCGCG CGACCGCCAC AGTGTAACTC AGCGCGCGCA AGGGCGACCA CTGATGAA	300
TTGGGGCGCA GTGTTCAAAG CTGGGGATA CGCGCGCCG CGTGAACAG CGTGGCGCT	360
TCGCTGGCTG CGCGCGCTT CTGGGGCTG TTGACCGATC CGACCGAC CGCGCGAC	420
ACCGACCGCG CGCGCGTAC ACCGACCTGC TCACCGACGC CGCGCGTT CGCGCGCG	480
TGCTGGCTG CTGGGGCGAC GAGGTGAGA TCGGAAATGC CGCGACAGCA CGGGTGTGCG	540
CGCGCGCGA CCTGGCTGCG TGCGTGGCG CGACCGCGCT GACGCGCG CGTTCACCC	600
CGGAAGCCAC CGCGCGATT CT	622

## (3) INFORMATION FOR SEQ ID NO:11:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGCGACGCG	TAACCCCTGTT	GGCGCGCGCG	ACACTGGTGT	TGACACCATG	GGCGCGGTGCC	60
ACCLACAGCT	CCTCGTCAGG	GGCGCGCGGA	ACGTTCTGGT	CGTGCGACGT	GGCGCGCGAC	120
AACGAGCTCC	ACTTCAGCGG	CTCGAACCGA	CAAGGAAATG	CCATGGACCA	TTTCGCTTAT	180
GCCTAACGTC	GATTCGCGCC	GGCTTACGCG	TTGGACTACA	ACCGCGACCG	GTGGCTTCC	240
CGCGTGACCC	ACTTTTCATA	CAAGGAAACC	GATTTACCGG	GCCTCGATGT	CGCTTTGATT	300
CGCTCGACCG	GTGAACTTCA	CGCGTCCGCG	CGCGCTTGG	TTTCCCGCGC	ATGGCGCTTG	360
CGACCGTGT	TGCGACGAT	CCGATGCTG	CGCGCTTGG	TTTCCCGCGC	ATGGCGCTTG	420
CTTCACGAC	CCACTACCGC	CAAGATTTC	AACGGCACCA	TCACCGTGTG	GAAGGATCGA	480
CAGATCCAG	CCCTCGACG	CGACACCGAC	CTGCGCGCAA	CACCGATTCG	CGCTTACGTC	540
CGACCGCAG	ACTTCGCTAC	GTGGACAAAC	TTCCGAGAT	ACCTCGACCG	TGTATCCAAC	600
CGCGCGCG	CGAAACCGCG	CAAGGAAACG	TTCAAGCGGG	CGCTGGCGGT	CGCGCGCGAC	660
CGAAACGAAACG	GAACGTCGGC	CTTATTCGAC	ACGACGACG	CGTCGATCAC	CTGACGACAG	720
TGATCGTTTG	CGCTGCGTAA	CGCTTGACAC	ATGGCGCGAA	TCATCACGTC	CGCGCGCGAC	780
GATCCAGTCG	CGATGACCGC	CGACTCGGTC	CGTAAGACAA	TTGGCGCGGC	CAAGATCGTG	840
CGACGACGCA	ACGACCTGGT	ATGGACACG	TGTTCTTGT	ACGACGACG	CGACGCTTGC	900
TGTTACCGCA	TGTTGCTGCC	GGCTTATGAG	ATGCTCTGCT	CGAAATACCC	CGATGCGACG	960
ACGCTCTG	CGTAAGGGCG	CTTATTCGAA	CGCGCGATTC	CTTCACGCG	ADGACCGTGC	1020
CGCGATACG	CGTCGATTCG	CTTACCGCGAA	TGTTCCGAG	CGAAATTCG	CGCGCGCGTG	1080
AATGCTATTT	CTTGACGCTG	TGAAACGAAAT	TGACCGCTGA	CGCGATCGGT	TCCGCAQSTA	1140
CGCTCGGAAAT	TTTGGCGCGTA	TCACGTTATG	CGCTGCTGCG	CGCGCGCGCG	GATGGCGACG	1200

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAACCCAGCT GCGAGTCGTC	60
CTTTGGACG AACTGGGAT GCGGAGACC AACAGCACA	
AGACCGCTA CGAACCGAT CGCGACGCCG TCGACTGTT GTTGGACAGG ACCCGGATC	120
CGTTTCTGCA AGATTTCTC GCGGACCGCG AGCTGACCGCG GCTCAAGGTC ACCGGTGGAC	180
CGTTGCTCCA AGCGGACCGCG GCGGACCGAT CGATGACG CACGGTGGAC CGAACCGATCG	240
CGCGGACCGCG CGGGTGGCG TCGACGGAC CGAACCGATCA GAACGACCGCG ATCGGCGACCG	300
ACCGGACCGCG CGGGTGGCG TCGACGGAC CGAACCGATCA GAACGACCGCG ATCGGCGACCG	360
CGGGGACCGCG CGGGTGGCG TCGACGGAC CGAACCGATCA GAACGACCGCG ATCGGCGACCG	420
TGTCGACCGCG CGGGGACCGCG CGGGTGGCG TCGACGGAC CGGGGACCGCG CGGGGACCGCG	480
CGGGGACCGCG CGGGTGGCG TCGACGGAC CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	540
CGCTGGTTA CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	600
AAGCGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	660
CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	720
CGCTGGTTA CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	780
CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	840
TGTCGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	900
AGCTGGTTA CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	960
AGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	1020
CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	1080
TGTCGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	1140
CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG ATCGGCGACCG	1155

## (ii) INFORMATION FOR SEQ ID NO:12:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGGCGGCGTC TGCGGTGTTTA AGCGGTTTAC CGGGGACCGCG CGGGGACCGCG CGGGGACCGCG	60
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GTGATGAAGG TCCCGGCGCA GTGTTCAAAG C

1771

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGGCGCGCG	GTGCGCGCGG	CCTCTTACACT	ATGTGATCCG	CCCGCGCTGC	GGAAATTGCGC	60
ACGAGGATCC	GACCTGGCG	CTTGTCGAC	CCCGCGCGGC	GGAAACTATCG	CTCCGATCCG	120
ACGCTTCCCG	CCGGCGCGCG	CCGATGGCG	CCGGCGCGCA	GGGGGGCAT	TTGCGCGCG	180
CCGGCGCGCG	CCGGCGCGCG	AAATGGCGCA	CTGAGGACG	GGGGCGAT	GGGGCGCGCG	240
ATCGAAATCAA	CTCTGATTCG	CCCTGGCGGC	CCGAGGACG	GGGGCGATG	GGGGCGCGCG	300
TGAAATGATCG	AAAACCGCGCG	CTGACGCTCG	CTGTTGACG	ATCGAGGTC	TCAGCCAAA	360
CTTGTGCGCT	ATCGAGGATG	TTTTCGCGCA	AACTGATGC	CGAGGAGCG	CGTGTTCGCC	420
TCAGCCAAA	GGCGTCCGAC	CCCGCGCTCG	TCGGCGAGT	CGGGCGATCG	CTTGATCGCA	480
CGAAAGCGTT	GGAGGCGCG	CCGGCGCTCG	TCGGCGAGT	CGGGCGATCG	CTTGATCGCA	540
TCGGTATTAC	GGATTCGCGAT	CTGGCGCTCG	GGGGCGCGCG	GGGGCGCGCG	AAGGGCGTAT	600
CGACCTACAA	CGACCGCGAC	CTTGTGCGCT	GGGGCGCGCG	GGGGCGCGCG	ATCTGCGTCA	660
AACTGTTCCA	CGACTGCGAC	AACTGCGCT	GGGGCGCGCG	GGGGCGCGCG	ATCTGCGTCA	720
TCGATCGCTC	CTGGCGCTCG	ACGGCGCTCG	TGTGCGCTG	CGGGCGCGCG	CGAGGCGCG	780
GTACCGCGCT	GTGAGGAGT	CTGGCGCTCG	GGGGCGCGCG	GGGGCGCGCG	CTTGATCGCA	840
CTGGCGCTG	CTGGCGCTCG	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	900
AGGAGGCGTC	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	960
TCACCGCGCT	GAATTCGAC	ACCTGCGCTA	GGGGCGCGCG	GGGGCGCGCG	GGGGCGCGCG	1020
GTGCGCTCGA	ACGGCGCTTG	GAACGCGTC	ACCTGCGCTA	GGGGCGCGCG	GGGGCGCGCG	1080

## (3) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

## (S) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGACAGCTGA TCGACATCAT CGCCACCCAC CGCACATCTT CGGACACGCC	60
CGCCCGGAG CGCTTCCACG CGCTTGCGA TAGCCTGAT GACATCCCGC TCGCTCGGT	120
CATTGACCG AGACATGCCG TGGACGCCG CGCGAGATT ACCTACCGCA TCGACCTGCA	180
ACTCTGTTT AACATGAGGC CGCCACCCAC CGCTTACAC CGCGCGCGA CGAGACCGA	240
AAATTCGACG GTTTCGTTT CATTGCGG ATTTTGTGTC TCGTCGCCA CGCTTACCGG	300
CGCGCGCA CGTCCCGTC CGCCCTATC CAGCGCTGA TCGCGATTCG CGCGCCACG	360
CGCGACTTAA TCGCTGGCT CGACCGAAC TCGCGATTCG CGCGCGACG TGTGCGTGA	420
CGTTCGCG CGCTTACAT CGCCCTTTC CGAGGAAAC GTGCTGCCAG CGCGTACGA	480
ACCGCTCCGA CGCGCGGTC CTGACCGCT CGCTTGCAG CGCGCGAGC	540
CG	542

## (ii) INFORMATION FOR SEQ ID NO:16:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGTTCGCG CGCGCGCTCGT TCGCGATTCG CGCGATGAGC TCGCGATTCG	60
CGCGATGAGC CGCTTGGCG CGCGCGACG CGCGCGCGCG ATGGTACCGC	120
TTCACCGTC CGCGCGCGCG CGCGATTCG ATTCACCGAC CGCGCGCGGG CGCGCTTAC	180
CGCGCTTACG CGCGCGCGCG CGCGATTCG TCGCGATTCG CGCGCGCGCG CGCGCGCG	240
CGAGCGCGCG CGCGCGCG CGCGATTCG TTCCCGCGCG CGCGCGCGCG CGCGCGATTC	300
CGCGACGCGCG CGCGCGCG CGCGATTCG CGCGCGCGCG CGCGCGATTC	360
CGCGCGCGCG CGCGCGCG CGCGATTCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	420
CGTTTGCAGCG CGCGACCGCG AGACCGCGCG CGCGATTCG TCGCGCGCG	480
CGCGAAACA AGACCGCGAC CGCGCGCG CGCGCGCG CGCGATTCG TCGCGCGCG	540
CGACCGCGCG CGCGCGCG CGCGATTCG AAATTTTATA AACCGCGACG CGCGCGCG CGCGCGATTC	600
CGCGCGCGCG CGCGCGCG CGCGATTCG CGCGCGCG CGCGCGCG CGCGCGCGCG	660

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ccccccccc cggcccccggc gtcggccggc tcccccgttt ggccgggtttt cccggccgttt 736
ttgttcctgtt caaggcctttta ccggccatttc ccgcggttcc ccggccggcc cccggccggcc 780
cccccccccggc ttggccgtttt accggacccggc ccgtggggcc cttggccggcc ttggccggcc 840
ttcccccgttt ccggccgtttt ccggccgtttt ccggccgtttt ccggccggcc 900
cccccccccggc ccc

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(3) INFORMATION FOR SEO IN MODULE.

#### 1.1 SEQUENCES, CORRECTNESS, TESTS

- (A) LENGTH: 1872 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

**(a)**) SEQUENCE DESCRIPTION: SEQ ID NO: 12

GATGAACTCG	CCACCCGGGA	TGGGGAGCGC	GTGTAACGGG	CATCATCGG	TTGACCGT	1380
CTGCGTGAC	TGGCAAACCA	AATCGGGCGG	CGCGGTACA	GGGAACUTGA	CTTCGGCGA	1390
GGACGCCCG	GGCTGATTG	TGGCGATAC	CGCGCGCGG	GGGGCGATT	GGATTGGCG	1400
CGGCGTGT	TCGGCGTGA	GGCGCGAGT	TGGCTTCCC	GTGGCGCTG	CGTTGGAA	1410
GCAATTAAC	AGCGAGAAC	CGCGTTGAG	CGCGCTCCG	TGCGGGCG	TTACCGGAA	1420
GGCGGTGCG	TGGCGATAC	GGATGCCAAG	GAATTCGCG	GGCGCGCGC	CGTCCCCCG	1430
GTGCGACG	GGTTTAAGG	CGCGCTTTC	TAGGAAGTGC	TTGTCGCGC	CTTCTTCAC	1440
GGCGCGCGG	ACGTTCCCG	GAATTCGTT	GGACTGATG	ATGGCGTCA	CTATCGCG	1450
GGGTTTGGC	TGACTGCGAT	CTTTCGCGC	GGTTCTTACG	ACTCGACCGT	GGCGACGGC	1460
GGTTCGCGA	TTGGCGATCT	CTGACCGTG	CTGCGCGAT	TGCGGCGCT	CGACCGTTG	1470
GTGCGCGCG	TGCGCGCTG	GGTTCGCGA	GGTTCGCGA	TGATCGCGCG	CGTCTGATG	1480
AATCGACCGT	CGGAGTCGA	CCCTGTTT	CGGGAGTCG	GGCGCGACCG	AGACCGACCG	1490
TACGTTGACT	ATTACCGTTG	GAAGGACACC	AGCGACCGT	ACATCGACCG	CGGGAGTCG	1500
TTCTCGACA	CGCGAGAGTC	GAATTCGTC	TTGCGTACG	TGCGGCGCG	CTTCTGATG	1510
CGACCGATTC	TT					1520

(2) INFORMATION FOR SEQ ID NO: 1a

## (3) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18.

CTTTCCGAA ACCTTATGCC GGGCAACCG CTGTTCGCGT GAGCCCTTACG CGCTTGAGC  
 60  
 CGCGCTTCT CGCCGAGATC AGGCACTCCG TTGTNTGGAC AAAACGGTTG ACCAGGATTC  
 120  
 ACCTTACCGT CGAACAAACC CGGAAACTCG ACAGCTTGCT GGTTATTACT ACTTCCGATG  
 180  
 TCGACCTTG GCGCAATCCG CTGGCTGCGA AGCGCGTATC GCGCTACACG GACGACCGG  
 240  
 CTGTTCGCGT TCGGGTACAA CGCACAAACG TCTCGGTGAA ACTTGTTCAC GACTGGAGA  
 300  
 ATCTCGGCTC GATTCTGAA CTGTCAGCTT GCGCGCTGT CGATCTCGT GCTGGGTG  
 360  
 CGCAGCTCT GTCCCGTTC AGGAACCTCC AAGCGCAAGG TACCGAACTG ATAGACCGAA  
 420  
 TTYCGAACGAC CGAAATGCC CGAACCTCC CGGAAAGCTC TGTCAAGATG CTTCGATCTG  
 480

CCCGGAGAC TGCAGGCCG GCAACCTTCG GATTCGCCA CGAACCTTG CAGGACTTG	540
TCCGAGCGC CATGGACCTC CGATCCGGT CGATTGAGT CGACGCTTG AAATGGACG	560
AACCCGTTAA CCTTGACTAG CGCGAAGTTG CGTGGACCGC TTGCTGAAA CGGCTTGTG	580
AACGGTGTCA AGCGCACCCG AAAACTGACG CGCTGACCGC ATCTGAAAAT TTACCGGTTA	600
GACCGGUCCG TTGGTGTGA TTCTTGCTG GTTCGGCGC GTCGACCGC CGCGACCTTG	620
CGCTTGTGA CGCGCTTG CTGCGCTTG AGGGCACTA CTTGCGCATG GTGGACGAGG	640
CGCTGATCA TGCGGCGCC AACCGATTCG TCCGCGCCG AARCTTGGCG CGCGGGCGT	660
AAGGCCTTAT TGAACGTGAC GATGAGCTG CGCGCTCAT ACCGGAGCGA CGCGCTTG	680
AAGGAAAGTG TTGGGCGTC CGCGTCAAAC GAAATTAAAC CGACTTGTC AACCGGCG	700
AGCGGATAGC CGCGAACCTC CGTGAGTTG CGTAGATTCG CGCGGGCGTG CGAGGTTG	720
CGGACCGTG CGACGATTC CGCGGCGTC CGGAGACCA CGCGTACCG CGCTGACAC	740
CGCGATATCG CGACGCTTAC CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	760
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	780
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	800
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	820
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	840
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	860
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	880
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	900
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	920
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	940
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	960
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	980
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1000
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1020
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1040
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1060
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1080
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1100
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1120
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1140
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1160
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1180
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1200
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1220
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1240
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1260
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1280
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1300
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1320
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1340
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1360
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1380
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1400
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1420
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1440
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1460
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1480
CGCGATTTA CGCGGGCGTG CGCGAGATG CGCTTCCCG CGCGGGCGTG CGCGGGCG	1500

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCCGCA CGACCGCGCG ATAGCTTCTG CGCCCGCGCG GACCAGATCG CGCGGGCGTT	60
CGCTGCTCGG CGACCGCGCG CGCGACGACG CGTGGACGCT GAGGACGCTG AACAGCGCGA	120
CGGTGACGCG TTGGCTCTCG ACCGGCGCGA CGCGCGCGTG CGTGGACGCTG ACCCGGGCGT	180
CGCGTACGCG ATCGGGCTACG TCGGGCGCG CGCGCGCGTG ACCGATGCGG CGAGGAGCGC	240
CGAGGAGACG TTGGCTCTCG CGACCGCTCA CGACGACGCG ACCGATGCGG CGAGGAGCGC	300

GUAGAACTTC GATCCTTGGG CCTCTCTGGG CGGTATCTAC CGTTATCAGG CGGCCAGGA	360
CGAACCCGCC AACGAGGAGCC AGATCTCTGGC CTCAAGGGTA GCGTCTTGG CGCGCTTAC	420
GGCAGGACAG ATCTCTGGCG CGCGCTTGGA TGTCTGGCC GACGTGTGGT CGCTGAGCG	480
TTCGGGGGAG CTAACCGGG ACCGGTGTGT CATCGAGACC GAGAAAGCTCC CGCGCTTAC	540
TGGCTGGGG CGCTCTCCCT ACCTGAGGAC ACCGCTGGAG AATGCTCTGG CGCGCTTAC	600
CGCGCTTACG GACTGAGTCG CGCGCTTACCG CGAACGAGTC CGACCTGGG TTGGGGGAG	660
ATACCTCTGG TTGGGGGAGG ACCGGCTTAC TTTTTGGGAC ACTCGGGGG CGCGCTTAC	720
TTACCTGAC CGCGACGGCG AATGCTGAGT TGTCTGGGT TTTGGGGGG CGTGCGGGCG	780
TGGACGGGTT AATATGAGCC CATTTGGGT CGCTCTGG CGCGCTTACCG AGTTACCGGG	840
ATTGGACCAA CGCTGGGGGT TGGGGGGGG TAACTT	876

## (ii) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCCCCGG CCTTCAAGAA TTGGGACCGA GAGACAAAAT TGGACGGGTT AATGAGGAA	60
CAGATTGATA ACCGAACTTC AGCGGACAA CGATATCTGG CGATCGGGGT TTATTTGAC	120
ACCGAAGACC TGGCGGTTT CGCGGAGAT TTTTACACCC AAGCGCTTAA CGGACGAAAC	180
CGTCGAACTA TTCTCTTCA AGCTTCTTC GACCGTACCC TTGGTGTGAA AATTTTGGG	240
CTAGGACCGG TGCGAAACCA TTGGGACACA CGCGCGGGG CGCTGGGT CGCGCTTAC	300
CGGAAACGCA CGTGCACCA CGCGCTGGT CGGTGAGGCG CGCTGGCCCG CGACGAGGC	360
CGTTGGCTGG CGCGCTGGAT CGCGCGGGCG CGACGCTGGT CGCGCTTAC	420
TTGATGCGAA CGCTGGTGG CGCGCTGGAT CGCGCGGGCG CGACGCTGGT CGCGCTTAC	480
AACTTGGTGG CGCTGGTGGT CGCGCTGGCG CGCGCTGGAT CGCGCGGGCG CGACGCTGG	540
CGCGCGGGCG CGCGCTGGCG CGCGCTGGAT CGCGCTGGCG CGACGCTGGT CGCGCTTAC	600
TGGAGATCGG CGCGCTGGAT CGCGCTGGCG CGCGCTGGAT CGCGCTGGCG CGACGCTGG	660
CGCGCGGGCG CGCGCTGGCG CGCGCTGGAT CGCGCTGGCG CGACGCTGGT CGCGCTTAC	720
CGCGCGGGCG CGCGCTGGCG CGCGCTGGAT CGCGCTGGCG CGACGCTGGT CGCGCTTAC	780

GGGTTGGCC CGAACCGGTT GGCACACTG CTGGCTGGT ATGGGGGGT CTTGGGAGC	840
AACAACTTG GCGAGGCG TGGACCGGC CGGATCGCA GACCGGCGG CGAAACCGA	900
CATCACACT GCGGGGATC GATGCGGGA GGGGGGTGG CGAAACCGA ACCGGTGTAG	960
GAGGCCAGC AGTTCCTTTT CCACGACCGA ACCGGTGTAG CGTCATCGG CGGTTTAAG	1020
T	1021

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCTGCCACG AACGGAAAGA CACAAACCTG AAGATGTTTA AATGGATCGC CGAACGTTTG	60
ACCGCCGCGG CTGCAATGCG CGCGCTTCCG CGCGCTTTCG CTTGGATCAT CGCTGGCGCN	120
CGCGCTTAT ACCGATCGA CGCGCTTCG TTGGCGCGCG CACTGGCTT CGACCGGAA	180
TCGGCGCTG AAGTGGCGCG CGGGCGGAG CGGACCGAGC TTCTCAACAG NGTGGCGAT	240
CGAACGTTG CGGCGAT CGGGCGAT CGGGCGAT CGGGCGAT CGGGCGAT CGGGCGAT	300
CGGGCGAT CGGGCGAT CGGGCGAT CGGGCGAT CGGGCGAT CGGGCGAT CGGGCGAT	360

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTAATGGT CGCGCTTGGC GACGGGTTTT CGGGGGGGT CGTTCACCGG CTGGCGCGT	60
CGATCGACCG CGCGCGAGAC CTGGACTCCG ATATCGCGC CGCGCTTGGC CTGGCGCGC	120
CGCTGGCTGT GAACTGGCGA CGCGCTGAAAGG ACCGGTTTA GACGGGGATC AAGGGCGTTG	180
ACCGGATGAC CTGGATGAC CGCGCGAGC CGCGCTGAT CGCGCGAGAC CGCAAGACCG	240
CGAAAACCG CGCTGTGTG CGACGACGAT CGTCAAACCA CGGGAAAGAA CTGGCGCGT	300
CGTGGCGATCC AAGAAGCGAG CGCGCTTGG TATACGTTGG CGATGGGGCA AGAAGGAA	360

CTTACCATCG CCC

373

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACACCCCT GATGGGATTTC CTGGGGGGGG CGGGTCCCTT CGGGCTTGTC GATGGGAAAC	60
TGGTTACCCG CGGGCGCTTA GCTGGTGTGT TTGGCTCAAGC AGGGCGTGTG CGGGTCTCTT	120
TCTTACCCG CGGGTACCGG TTGGGGGATT TACCCCGAGAT CGGGGGGGGC GAATCGTTC	180
TTATTCATGC CGGGTACCGG GTGGGGGCA TGGGGCTCTT CGGGTGTGT CGGGGGGG	240
CGGGTGTGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT CGGGGGGGT	300
TTGGACGACGA CGGGGGGGGG CGGGGGGGGG ACATGGGAGG TTGGGGGGCA GA	352

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGGG TTGATTTCTT TCGACCGGGG CGGGCGATA ATOGACCGAG TGTATGGCC	60
CGGGTTGGGG CGGGCGATGGG CTGACGAGGA GAAATCGGGG AGTTCTCTGG TATATCGAC	120
CTAACCGTCCA TTGGCTTGGG AGATGGGTTT CGTACGTTCA TGGCTGTAC CGGGTGGGCT	180
GGGGCGCTT CGTCTGGGGG TGGGGGGGG TGGGGGGGT CGGGGGGGT	240
GGGGGGGGT CGTCTGGGGG TGGGGGGGG TGGGGGGGT CGGGGGGGT	300
CTTTGGACCC CGGATGGGGG CGGAGCTGGG ATGGCTACAC CTGGCTTGAC GACTTGAC	360
GGGACGGGGA CGGGGGGGAC CGGGGGGGG ACTGGGGGGG ACCGATGTC GAGGGGGGG	420
TGGTGGACGA TGGGGGGGGT CGGGGGGGC CGGGGGGGT CGGGGGGGT CGGGGGGGT	480
CGGGGGGGG CGGGGGGGG CGGGGGGGG TATTAACGGG GGGGGGGGG CGGGGGGG	540
CGGGGGGGG CGGGGGGGG TTGGGGGGG CGGGGGGGT ATGGGGGGGT CGGGGGGG	600
AAAATGGGGG CGGGGGGGG CGGGGGGGG GGGGGGGGG CGGGGGGGG TGGGGGGGG	660

GCGGACAGCG CCTGGACGAT CGACATGGAC AACGTTGTTA CGGGCACACC CGTTCGCCGG	720
ATGCTG	726

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCGGACAGCG AGCAACGATG CGGGCACACC CGGCTTAAGG TTGATGGAG CGATGGGAT	60
CCTGGCGGC CGATTCGAAG GATGCTGGGT CGACATGGAC AACGTTGTTG CGGGCACACC	120
CTGGCGGTG CGGGCGGTTG GAACTTATTG CGGGCGGGGT TGTGACCTTG ATGAACTCAA	180
ATAGGGAACA ATAGGGCGTT GATTTGCAAG TTGATGTTGG CGTATGGCTG GAACTTAAAT	240
CGGGGGCAT CGTCGCGGACG GACCACTTC CGGGCGGCG CGAACCGCGA ATCTTGAGCG	300
ACGACTTAAAT CGGGCGGATG AACGTTGGAA CGGGCGGCG TGTGTTGGAA GCAACTTAACT	360
ACGGGGCGCG CGATTCGAATG CGAATGGCGAC TTGAGGCTGG CGGGCGGCG GTGTTGAGCT	420
TGACACCCGA CGAACCGCGC CGACTTGGTG ACCGACTCAA ACCGGTTAACT AGCTTAAGCC	480
ACGGGGCGCG CGATTCGAATG CGGGCGGCG CGAACCGCGC CGGGCGGCG CGGGCGGCG	540
TGGGGATTT ATGGCGGAGGA GAACTTGGTG ATAGGCGCT	600

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGCGCG CGGGCGGTTT TGCGGGCGGT CGGGCGGCG CGGGCGGCG CGGGCGGCG	60
CGTACCGCGG CGTATGGCGG TGTGCGGGCGG CGGGCGGCG CGGGCGGCG CGGGCGGCG	120
CGGGCGGCG CGTACCGCGG CGGGCGGCG CGGGCGGCG CGGGCGGCG CGGGCGGCG	180

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA	CGATGGTGTAT	GTACGCCAAC	GTTTTCGACA	CCCTCGAGGC	GTTCACCGATC	60
CACGCCACAC	CGGACCGCT	GACCATGGC	GTGGCGGCC	GTTCGCGGA	CCGGCTTCCC	120
AAGGGATGG	GAATGACAA	CTTCGGGTA	ATTCTTACG	GAATGGACCC	CGTCGTGCTT	180
GAACCTGAAAC	ACTGGGAGGA	CGGAAACAAAC	ACGTTGGCGT	TGGCGCCCG	TGGCGTTC	240
CCCTACGGC	CGAACGTTCA	CGGAAACGGCT	CG			372

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGACCCGTC	GTTCCTGGAC	TATCTGGCA	CGTTCACCA	CGCGGACGTC	CGCGACGTC	60
ACCAGATGCA	CGAGACGGAT	CGCTTCGCC	GTTCATGCG	CTACCTGGC	GTATTCACCG	120
CGCGGGAGCT	GAACGGGTC	CGTCATGCG	GTTCGACCG	CGGACGATCC		180
GTTCGGATCT	CGCTTCGTC	CGTCATGCG	GTTCGACCG	CGGACGATCC		240
CGAAATGAC	CGCGGAGTC	AAAGACCGCT	CGAAGATCCA	CGTCGTGCG	ACTTGCTTCG	300
CGCGCTTCTT	CGCGCGCG					317

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG	CTTCGGATCA	ACGCGGTTTC	CGGACGGGCG	CGGGCGAGCA	CGTCGGTTC	60
CGAAGCGCGG	ACCGCTGGCG	CGCTGGCGAC	CGTCGTGATG	ACCGCTGGCG	CGTCGGCGAC	120
CGCTTGGGCC	CGCTTACGAA	ACGCGGCGAC	ACCGCTGGCG	CGTCGGCGAC	ACGCGGCGAC	180
CG						183

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATGCCGAG TTTGTGAGC AGGTGCTCGA CGCGAAATTC TGCGCCGCTG CGAAGCGCTT	66
CGCGCTTAC CGGGGAAAGA CACCGCTTCG CGACCTCTTC CGCGCTCTTG ACGGCGGCA	126
GAGGTTUAGA TTGGCGCGCG CGCGAACCGG GTGGAAAGC TTGTGGCGCT GCATTTTAT	186
CGACCGCC CGTTTAATTC TACCGACCG CGTGTACCGG TCCCGACGAA TTTGGACCT	246
CGGTTGCG ACCACCTCT CGAACGTTT CGGGGAAAGA CGCGAAATTC ATGGACGCC	306
ACGTTTGG	308

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGAACGCGA CGACGACG TCGATCTCG TCGCGCGCG CGTGAAGAC CGAGAGAATC	66
CGGCCGAAGC TCGCGCGCG CGACTCTCA TACTGACCGG CGTGAAGAC CGCGCCCCGAT	126
GGCACCGGAC TATTCGTTG TCGCGCGCG CGTGAAGAC CGTGAAGAC ATGTGAGGGG	186
ACACGATCG CAATCACACG TACCGACGCA TCGAGATCTG CGCGACCTCG CGCGACCGCG	246
TGCGACCGCG AATCCGAGGC CGTCTCG	267

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGCTGCCGA AAGAAATCTGA CGGGACACGA TGAGCAATCA CACCTACGA GTGATCGAGA	66
TCGTGCGAAC CGTGCCTTAC CGCGTCTCG CGGCAATCGA CGCGATCTG CGCGGAGCTG	126

CACAGACCAT GCGCGCGCTG GACTGGTGC AACTACAGTC AATTCGAGGC CAGCTTGCG	180
ACGGAGCCGT CGCGACATTC CAGGTTGACTA TTTAAAGTGTG CTTCGGCTCG AGGATTCTG	240
AACCTTCAAG CGCGCGAT AACTUAGGTG CTCATTTAGC CGACTTTTTC AGAACATCT	300
GACCGCTCG AAACCGGTTT CAGCCGACCG TCGCTTCCC GAGCGCGCTG CTCCAAAATC	360
CCCTGCCAGCA TTTCGCGCC CGCGCTACCA CGAGCTGCTG CCTGAATTGC TCGCTTATCT	420
CGTGGACCTG TTTGGCTTC AGCCGGACGA AGCGGTCTTC GACGCGCTT CGCGCTGCG	480
CGCGATGGG TCGCGCTCA CGCGCTATCTT GAAACAGGGAG CGACGCTTCG CGCGCTGCA	540
TATCTCGAG AAGCGCATCG CGTCGCTCC CGCGACATTC ACCTGGCGCC ACCCGCATTT	600
CGCGCTCG CGCTCGCGCA TCTACGACTC CGTCGCTCC CGCGACATTC AATACCGATC	660
ACTTGACTTT CGTTTTGCGAT ATCCGGATCC CGCTTGTGAT CGCGCTTTC TTACCGCGT	720
GTTCACCCAC ATTTTTCCCG CGGACGCTGA CGCTATCTG CGCGACATTC CGCGCTGCT	780
GAAGCCCCGC CGACGATGCC TGTGGCGCTA CTTCCTTCTC AATGACGAGT CGTTAGCCCA	840
CGTCGCGCA CGAAAGACGT CGCGACATTC CGACGATGAC CGCGCGCTT ATCGGACGAT	900
CGACAAAGAG CGCGCGCGAG AAGCGATCCG CTTCGGCGAG ACCTTGTCA CGCGCTGCA	960
TGCGACGTT CGCTCGCGCG CGCTCGCTCC CGCGACATTC ATTACCGCGT	1020
ACCGCGCTTA AGCTTCGAGC AGCTCGCTAT CGCGACGCAA ACCCGGAGCT AGCTCGCTAT	1080
CGCGCGACCA TGGCGACATCT CGCTCGCTCC CGCGACATTC ATTACCGCGT	1140
CAGATTAGCC CGCGCGCTT CGCGACATTC AATACCGCGCC CGCGACATTC CGCGCGCTT	1200
GGTAACCGG CTTCGGCGCC TGGCGACCG CGCTCGCTCC CGCGACATTC ATTACCGCGA	1260
ACCGCGCTG ATCGCTGATC ACCGAGCTG ACAGCGACCG CGCTCGCTCC ACCCGCGAT	1320
CGACCGCGCTT CTCCGGCTCT CGCGACGCAA TCGACCGCGCC CGACCGCGCA TGACCGACG	1380
CGCGCGATCAC TTTCGCGATC CGCTCGCTAT CGACGCGAG ATGAAAATTT ATCGGACGAT	1440
ATACGATTTGC ATCCGGCGAGA ACTTGACGTCG CGCTCGCTT CGCGCGCTG ACCCGCTCC	1500
CGCGACGCAA CGCTCGCGCG CGCTCGCTCC CGCGCGCTG	1560

## (2) INFORMATION FOR SEQ ID NO:33:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGCGC	GGTGTGATCA	GCTTCACCCG	GGGCGGCC	GACCTGACCC	CAGGCGGTT	60
CGGGCTCT	GGGGCGGCT	ACGAGACGCC	GTATGGGCTG	ACGGTGCGCC	GGCGCGTGAT	120
CGCCGAGAAC	CCTGCTGAAC	TGATTTTCTT	GTACCGACCC	AACCTCTTGG	GGCAAAACAC	180
CGGGCGATC	GGGTCAACG	AGGCGGATAA	GGGGAGATG	TGGGGCCNAG	ACGGGGCGGC	240
CATGTTTGGC	TAGCCCGCG	CGACCGGAC	GGGACGGG	ACGGTCTTC	GGTGGAGA	300
GGGCGGGAG	ATGACCGACG	CGGGCGCT	CTTGAGCACG	GGGGCGGGCG	TGAGGAGG	360
CTGGCGACCC	GGGGCGGCCG	ACGGTCTGAT	GAACAATGTC	GGGGCGGCG	TGAAACGTT	420
GGGGCGATC	ACGGAGGGCA	CGGGCGCTC	TTCGAAGCTG	GGGGCGCTGT	GGAAAGACGGT	480
CTGGCGCGAT	GGGGCGGCCG	TGAGGAGAT	GGTGGCGATG	GGCAACAAACC	ACATGGCGAT	540
GGGGCGGCG	GGGGCGGCCG	GGGGCGGCG	CTTGAGCTCG	ATGTTGAGG	GGGGCGCTGC	600
GGGGCGGGG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	660
GGGGCGGGG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	720
GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	780
GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	840
GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	GGGGCGGCCG	900

## (D) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CATGGATGG	GGGGAGATTT	GGACCGATT	GGGTTGCGC	GATAACCAA	TGATGGGAG	60
CTAGGTTAT	TGGGCGGAG	GGCCCGAGTA	ATGGCTCGCA	GGAGGGGAC	GGTACTGGTC	120
GGGGCGGCC	TGGTGGGTC	TGGTACCGCC	GGAAAGCGTC	SACATTTGCC	ACGGACACCC	180
GGGGCGGCC	GGGGCGGCC	GGGGCGGCC	GGGGCGGCC	GGGGCGGCC	GGGGCGGCC	240
GGGGCGGCC	GGGGCGGCC	GGGGCGGCC	GGGGCGGCC	GGGGCGGCC	GGGGCGGCC	300

## (D) INFORMATION FOR SEQ ID NO:35:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC	GAAGCCGGCG	CCTCCCAAGGC	GAAGTCGCTG	TTCGACCCAGG	AGGGACCGGA	69
CGATCTTCCC	CTTCGGATCG	CGGTTCAAGCC	CGGGGGCGTC	GTGGGATTTC	GTATAAACCT	126
TTTCCTTCCCAC	GATCCGACCC	TGGATGTTTA	CGAAACCGG	GAATTCCTT	GTGTCAGGTT	183
GATCCTGACC	CGATCTTCCC	CGGGGGCGTC	GAAGTCGCTG	TTCGACCCAGG	AGGGACCGGA	240
TATTCGAGAG	CAAGGTTTAC	CATGCGCAT	CGTAAACCGG	TGGATGTTTC	TCTTCACAC	300
GATTCGTTCA	ACTGATAAAA	CGCTTACCG	AACCGGGCGT	GGCGAACACG	TACCGAGGAC	360
CCAAGACCTG	ACCGGGCTTG	AAAGGCACT	GAACGATGCC	TTTCGACTGA	CGCGCTGGCG	420
CGCCCGCCAC	CGGAGGTGTC	ACCTTCCTTC	TGAACGACAC	CTTCGCTTGA	TATTCGGACC	480
ACTACACCAT	TTTGTGCGTC	GAAGTCGCTG	CGATCTTCCC	GAATTCCTT	CGGAACCGGT	540
CGCTTCTTCA	TTTGGCCCAAG	CGCTGATGG	AGGGGTTTC	GGCGACGGGG	TGGTGGATAC	600
CGCACACCGC	ATTGGGAAAC	ATGGTGTCA	CGTCGGCGTT	CTGGGACCGG	TTGAGGTATC	660
CTCTGATTCG	GGTTTTGGCC	GGTCCTTCCG	AGAATGTCGC	TGGCTTGTTC	CTTCGCTTGC	720
TGCGGACCCC	GTATATGATC	CGGGGGCGTC	TAGCCGACAC	CGGGGGCGTC	GTACACCGAA	780
TCCTGATTCG	CGGGGGCGTC	TCGGGGCTTC	TCGGGGCTTC	CGGGGGCGTC	CGGGGGCGTC	840
GATTCGTTCA	CGGGGGCGTC	TCGGGGCTTC	CGGGGGCGTC	CGGGGGCGTC	CGGGGGCGTC	900
CGGGGGCGTC	TCGGGGCTTC	TCGGGGCTTC	CGGGGGCGTC	CGGGGGCGTC	CGGGGGCGTC	960
ACGGGGCGTC	TCGGGGCTTC	CGGGGGCGTC	TCGGGGCTTC	CGGGGGCGTC	CGGGGGCGTC	1020
TTCTCTTGG	GTGGTGGACG	CGGGGGCGTC	TCGGGGCTTC	AACGGGGCGTC	CGGGGGCGTC	1080
CGGGGGCGTC	TCGGGGCTTC	CGGGGGCGTC	TCGGGGCTTC	CGGGGGCGTC	CGGGGGCGTC	1140
CTCGAACCGG	CGGGGGCGTC	TCGGGGCTTC	CGGGGGCGTC	CGGGGGCGTC	CGGGGGCGTC	1200
ACGGGGCGTC	TCGGGGCTTC	CGGGGGCGTC	TCGGGGCTTC	CGGGGGCGTC	CGGGGGCGTC	1227

## (2) INFORMATION FOR SEQ ID NO:36:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGTGTCGCG CGGATCGGC CGCTTGTTGA ACCGCAACGG CGGGGTTTCG GGGGGCGCG	60
GGACGGCGCC TAACTCTGGT CGCGCGCGCA ACCGCTGGTT GTTGGGGGCC GGGGGCTCG	120
GGGGGGCGCG CACCAATGGT GGAGGCGCG CGTCCGGCG ATTGGCTAC GCGAACGGCG	180
C	181

(2) INFORMATION FOR SEQ ID NO:37:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGTGTCGCG CGGATCGCGT CGGTGGTTGA ACCGCAACGG CGGTGTCGGC GGGGGCGCG	60
CGGAGGGCGT CTTTGGCGGT CGCGCGCGCC ACCGGGGCGGT CGTGGCGCG CGCGCGCG	120
CGGGGGCTC CGACCGCGT AACGGGCGTC TTGGGGCGGT CGGGGGCGGC CGACGGCG	180
CGGGGGACGG CGTGGCGGT CGGACGGCG CGTACGGTGG CGAGGGCGCG ATTGGGGCG	240
CGACTGAGAG CGGGGGCGCG CGTGGGGCGT ACCGGGGCGTGA CGGGGGCGCG	296

(3) INFORMATION FOR SEQ ID NO:38:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCACCG CGTGGGGCGT CTGACTCGAA CGAT	34
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(2) INFORMATION FOR SEQ ID NO:39:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGCTCT CGTCGCGCCG TTGGCGGAA CGCCACCGTT CGAACGTTA CGGACGAGC	60
TGCGGTGTC GGCAGCAAGC CGGGACGCC CGACCGGA CGCGACAT CGACCGTGC	120
TATCGCCAC ATTGGCGCG GNCGACGCCG CACCG	180

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGCCGTTTA CGGGCGGCCG CGGACGCCG AGCCCGGNG CGCCCGCGCG TGC	93
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## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCGACCG CGGTGCGAAC CGTCGCGCC CGCCACGTT GACCGCCGC CGCAACGGCG	60
CGACCGCCG CGACCGCCG AACCCGACG TCGCGCGG CGCCCGCGC CGACCGCCG	120
AGGCCCGGCA CA	180

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGCGCGC CGGACGCCG GCGACGCCG GCAAGGGCGG AAACCGGGCG CGCGAGCTCA	60
CGCGCGAGA ATCGTGGCG TGCGCGATG CGCGCGATG CGCGACGCCG CGCAACGGCG	120
CGACCGCCG CA	180

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs

- (S) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCGCGGCGGC ATGGGTACCC CGCGGCGATCG CGACGCTGCCG ATTGGCGCGCG TTTCGCCCCAC	60
CGACGGAAAC CGTTCACCGA TGCCGCTTCCG GAAATAGGGC GATCGCGTTTG CGATGCCGGC	120
ATGAACGCGGC CGCCTTAAAT TACTGCGCA ACCTTTTCACT TTACCGCGCA TAATGGCTAT	180
AGCAGCTTACG AGGATGATCC GATATGACCC AGTCGCGAAC CGTGCACCGTG GATCAGCGAG	240
AGATTTTGAA CGGGCGCAC GAGGTGGAGG CGCGATGGC GGACCCGACG ATGGATGTC	300
CCATCGACCG CTGGCGACTC ACGGNGGTTA AAAACCGGGC CGAACAGTC CGTTTGTCCG	360
CGGACAACAT CGCGGATAC CTGGCGCGCG CGTCCGAAGA CGCGCGCGCT CGGGGACCT	420
CGCTGGCCAA CGCGGCGAG CGTATGCGG AGTTGATGA CGGGCGCTCG AGCGCGCTCG	480
ACGACGACCG CGAAGGACT CTGCGACCG AGTGGCGCG CGCCGCTCGA CGCGACGTT	540
CGGGCGACT AACCGTACG CGGAGCGTG CGCGCGCG CGAACCACCG TTTCAGGATC	600
TCAAAGGAGC CGCGGCGAG CTGCGAACCG CGCGCGCG CGCGACGTC CGCGCGTGC	660
CGCGTGCCTG CGAGCTTACG ACCGTTACCC CGTCAAGGTA CG	720

## (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCTTGAC CGCTTGCGCG CGACGCTGCCG CTGCGACCG CGTGGCTCG TGCGTTTGG	60
CGCGCGCGCG TGCGTTTGGC CGCGCTGCCG TGCGCGATCG CGCGCGCGCGA ATCGCGCGCG	120
CGCGCGCGCG CTGCGACGAT TGCGCGCTTA CGCGGCGAA CGCGCGCGCG CGCGCGCG	180
CTGGCGCGCG CGCGCGCG CGTGGCGATG CGCGCGCG CGTGGCGATG ATCGGGGACG AGCGCGCGCC	240
AAGTCCGAGG GTTGTGCGA CGAAGGCGAG CGCGCGCGA CGCGCGCG CGTGGCGATG	300

## (2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAGCACCGAGG ATCGAATCCC CTCCTCCGAA GCACACCCTC GCACTGCACC AGTGCAGGAC	60
CCATGACCTA CTGCCCCGGT AACGCCGAAT ACCCCCAAGC GCAACGGGCA GGCCTCTAAC	120
GAGGCGTCAC ACCTCTTTG GCGCGCCCG ATGAGGCTAC GCGGAGCTA CCCATGTACG	180
TGAACATCCC CCTTGCGACTG CTGCGTTGG CTCGCTACTT CGCCCGTTG GGCACCATGT	240
TGACCTTGAG TACGGGACTC GGCGGGGTG ATGGCCGAT GTCCCGTAC ACTGGGCTCC	300
CGCTCGGT CGCTCTGCTG GCGCGCTAC TTGCGGGGTG GGTTCGTTG CCTAAGGCCA	360
AGAGCCATGT GCGGTAGTT GCGCTCTCG CGCTACTCG CGTATTTCG ATGGCTCGG	420
CGACCTTTAA CGAGCCCGCC CGCTATTGCA CGCGTTGGGC ATGGTGGTT GTTGGCGTT	480
TCATCGTTT CGAGGGGGT CGCGCTAC CGCGCTTGGT CGTGGAGAC CGCGCTATCA	540
CGCGCTCGAC CGCGCGCCG AGCTTGACG CGTATGGACA ATGGCGGCG TACGGGAGT	600
ACGGCGCTTA CGGGTGGAG CGCGCTGGT ACTACGGTCA CGCGCTGGT CGAGAGGCC	660
CGGGACTGCA CTGGCGGGC CGCGCTAC CTGGCGAGCC TCGCGGATAT CGTGCCTGTT	720
ACGGCGCTTA TTGGTGGCT CGCGCTGGT CGCGCTGGT ATGGCTGGT CGGGCGGGG	780
CGCGCGCTCG CGCGCTAC CGGTGCGAAC ATGGCGGCA CGCGCTGGT AGCGCGCTTA	840
CGCGCTGGT CGGGTGGAG CGCGCTGGT CGCGCTGGT CGGGCGGGT CGCGCTGGT	900
CGTGGCTGGT ATGGCTGGT CGGGTGGAG CGCGCTGGT CGCGCTGGT CGGGCGGGT	960
CGGGCGGGT CGGGCGGGT CGGGTGGAG CGGGTGGAG CGGGCGGGT CGGGCGGGT	1020
CGGTGCTGGT AGGGCGGGT CGGGCGGGT CGGGCGGGT CGGGCGGGT	1080

(ii) INFORMATION FOR SEQ ID NO:46:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGTCACCGAGA GACCGATGCC CCTAACCTCG CGCAGGAGGC AGCTAATTTC GACCGATCT	60
CGGGCGACCT GAAACCCAG ATGGACCCAG CGTGGTGGAC CGCAGGTTAC TTGCGGGCC	120

AGTGGCGGCG AGGGGGGGGG AGGGGGGGCC AGGGGGGGGT GGGGGGGGTTT CAAAGAAGCG	180
CCAAATTAAGCA GAAGCAGGAA CTGGACGAGA TCTCGACGAA TATTCGTCAG GCGGGGGTCC	240
AATACTCGAG GCGGGACGAG GACCGACGAG AGGGGGGTTC CTCGCGAAATG GCGTTTGAC	300
CGGGTAAATAC CAAAAGAAC CGGGCAA	327

## (2) INFORMATION FOR SEQ ID NO:47:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGCTCGGGAT GATGGCGTTG TCGAACGCTGA CGGATTCTGT ACCGGGGTGG TTAGAGATCAA	60
CCAACAAACGT GTTGGCGTTC GCAAAATTCGC CGGACGGTGG GATCTGGGTC ATCTTTTGT	120
TCTTCATCGAG GAACTGCACA CGGGGGACCC TGGCTCGGN TACCTTTGGG	176

## (2) INFORMATION FOR SEQ ID NO:48:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCCCGGG CACGGGGGT GCGGGGGGCA CGACGGGGTG CGCTGGGGGGG AACGGGGGGG	60
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	120
CGGGCGT	137

## (2) INFORMATION FOR SEQ ID NO:49:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGGGGGGAG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCA AGGGGGGGAA	60
CGGGGGGGTG CGGGGGGGAC	81

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGCTT GCGCGGCTCC CGCCGAAACG CGCGTAACGG AGGAGCTGCC GAAATTGTTTC	60
GCAACGGCGG CGCGCGGCGT CGCGCGGCGT CGAACCGAGC CGGTAAACGGC GGCGCGGGCG	120
GAAGACGGTGC TCGCGGTGGG CTCAGATCG	149

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCAAGAGA TCAAGCTTAC CGAGTGATCG AGATCGTGG GACCTCGCGG GACGTTTGGC	60
ACCGCGAAAT CGAGGGCGT CTGGCCCCAG CTGGCGAGAC CGACCGCGCG CGTACGTTT	120
TGAAACTACA CTGCAATTGA CGCCACCTCG TCAACGAGC GGTGGGGCAC TTCCAGGTTA	180
CTATGAACT CGCGTTTCCC CTGGAGGATT CGTACACCTT CAAGGCGCGC CGTACGTTA	240
CGTGGCATAT TAAAGGACTT TTGGAGAAC TCTTGACCGG CTGGAAACCC GGTGGAGCG	300
ACGGTGGTC CGCGCGGCG CGCTCGAA AATGGCTTAC AGAATTGTC CGCGCG	355

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATCCATGACC ATCACCGTCA CATCACCGAG GTGGACCGCA ACTTGACACG TCGAAAGGG	60
CGATTCGCG CACTGGCTAT CGCGCGATG CGCGCGCGCA CGCTGGTGAC CGTACGCGTC	120
CGCGCGACCG CGAACCGCGA TCGAGAGCA CGCGCGCGCG TACCCAGAAC CGCGCGCG	180
CGCGCGCGCA CGCGCTGACG CGACCGCGCA CGCGCGACACG CTGTTTGCGCG CGCGCGCG	240